

GenCore version 5.1.6
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oleic search, using sw model

February 29, 2004, 19:44:23 ; Search time 10058.5 Seconds
(without alignments)
17262.293 Million cell updates/sec

US-09-424-686F-9
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IDENTITY NUC
Gapop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues
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length: 0
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Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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is the number of results predicted by chance to have a

score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
AX001446
LOCUS AX001446 4042 bp DNA linear PAT
DEFINITION Sequence 1 from Patent WO9859040.
ACCESSION AX001446
VERSION AX001446.1 GI:7241612
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4042)
AUTHORS Wick,M. and Hagen,G.
TITLE HUMAN CATALYTIC TELOMERASE SUB-UNIT AND ITS DIAGNOSTIC /
THERAPEUTIC USE
JOURNAL Patent: WO 9859040-A 1 30-DEC-1998;

: 09:53:29 2004

us-09-424-686f-9.rge

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ACCESSION	AX003121				
VERSION	AX003121.1	GI:9926983			

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MARESA (DE); BAYER AG (DE)
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Conservative 0; Mismatches 0; Indels 36; Gaps 1;
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ization thereof and structure and function of chromosome end.

6185.1 GI:23231130
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entified
entified
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n. G.: Siegmund, H. U., Weichel, W., Wick, M. and Zubo, D.

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19-MAR-2002

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DMITRY ZUBOV

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utilization

[illegible]

Location/Qualifiers

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Location/Qualifiers

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 4037)
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase
drug screening
JOURNAL Patent: US 6617110-A 343 09-SEP-2003;
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REFERENCE
AUTHORS
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,
Harley,C.B. and Andrews,W.H.
TITLE
Human telomerase catalytic subunit
JOURNAL
Patent: EP 133094-A 343 06-AUG-2003;
Geron Corporation (US) ; University Technology Corporati
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ORIGIN

Query Match 98.5%; Score 3946.6; DB 6; Length 4037;
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RESULT 8

BD011070
LOCUS Human telomerase catalytic subunit.
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011070
VERSION BD011070.1 GI:18639443
KEYWORDS JP 2001081042-A/27.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4037)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 27 27-MAR-2001;
GERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 2001081042-A/27
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/84
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R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, I
MORIN.
PI CALVIN B HARLEY,WILLIAM H ANDREWS
PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00
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FH Key Location/Qualifiers

CDS

Location/Qualifiers

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98.5%; Score 3946.6; DB 6; Length 4037;

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Conservative 4; Mismatches 3; Indels 36; Gaps 1;

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QY	1328		AGCCGGTGTCTGTGCCCGGAGAACCCAGGGCTCTGTGGCGGCCCCCGAGGCA
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sapiens (human)
sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

s.C.J., Kipling,D.G., Wilkinson,G., Mosharry,B.D. and
ner,J.W.
lines, their preparation and use
nt: WO 0216555-A 1 28-FEB-2002;
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Location/Qualifiers
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98.2%; Score 3933.4; DB 6; Length 4070;
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Conservative 0; Mismatches 1; Indels 36; Gaps 1;

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4587 4015 bp DNA linear PAT 14-FEB-2001
ence 224 from patent US 6093809.
4587
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own.
own.
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98.2%; Score 3933; DB 6; Length 4015;
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2221 4015 bp DNA linear PAT 20-APR-2002
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2221.1 GI:20225137

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GenCore version 5.1.6
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February 29, 2004, 19:45:38 ; Search time 8119.94 Seconds
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US-09-424-686F-9

4006

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ubov, Dmitry
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; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
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; FILE OF INVENTION: Use
; FILE REFERENCE: Bayer 10,203
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; CURRENT FILING DATE: 1999-11-29
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4021 AAAAAAAAAAAAAAAAAAAAAA 4042
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RESULT 4
US-09-582-246-2
; Sequence 2, Application US/09582246
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the
; TITLE OF INVENTION: Subunit, and Their Diagnostic and Therapeutic
; FILE REFERENCE: Lea 32 805
; CURRENT APPLICATION NUMBER: US/09/582,246
; PRIOR APPLICATION NUMBER: 2000-09-21
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-582-246-2
Query Match 98.9%; Score 3960; DB 24; Length 4042;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 4006; Conservative 0; Mismatches 0; Indels 36;
QY 1 GTTTCAGGCAGCGCTCGTCTCTGCTGCGACGTCGGAAGCCCTGGCCCCGGCCA
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Db 61 CGATGCCGCGGCTCCCCGCTGCCGAGCCGTCGCTGCCCTCCCTGCTGCGCAGCCACT
QY 121 AGGTGCTGCCGCTGGCCACGTTTCGTCGCGCGCTGGGGCCCCAGGGCTGGCGGC
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QY 181 AGCGCGGGACCCCGCGGCTTTCCCGCGCTGGTGGCCCCAGTCCCTGGTGTGCG
Db 181 AGCGCGGGACCCCGCGGCTTTCCCGCGCTGGTGGCCCCAGTCCCTGGTGTGCG
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Db 241 GGGACGCACGCGCGCCCCCCCCCGCCCCCTTCCCGCAGGTGTCTCTGCTGA
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Db 361 GCTTCGCGCTGCTGGACGGGGCCCCCGGGGGCCCCCCCCAGGCCCTTCAACACCA
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Db 421 GCAGCTACCTGCCCAACACGGTGACCGACGCTGCGGGGGAGCGGGGCGTGGG
QY 481 TGCTGCGCGCGTGGGCGACGACGTCGTGTTTACCTGCTGGCACGCTGCGCGC
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Db 3781 TCCATCCCAGATTGCCATTGTTTCAACCCCTCGCCCTGCCCCCTCTTGGCCTTCC
Qy 3805 ACCATCCAGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTGGAGT
Db 3841 ACCATCCAGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTGGAGT
Qy 3865 AGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGAGGGGTCCCTGTGG
Db 3901 AGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGG
Qy 3925 TTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTT
Db 3961 TTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTT
Qy 3985 AAAAAAAAAAAAAAAAAAAAAA 4006
Db 4021 AAAAAAAAAAAAAAAAAAAAAA 4042

RESULT 5
US-08-974-549-343
; Sequence 343, Application US/08974549
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 726
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:

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QY 2972 TCACAGCCTGTTTCTGGATTTGACAGGTGAACAGCCTCCAGACGCTGTCACCAA
Db 3001 TCACAGCCTGTTTCTGGATTTGACAGGTGAACAGCCTCCAGACGCTGTCACCAA
QY 3032 CAAGATCCTCTGCTGCAGGCGTACAGGTTTCAAGCTTCAAGCTGCTGAGCTCCC
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 3 GCAAGTTTGGAAAGAACCCACATTTTTCCTGCGGTCACTCTGACACGGCCTCCCT 3180
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 9 CCTCTGCCCTCCGAGSCCGTGCAGTGGCTGTGCCAACCAAGCATTCCTGCTCAAGCT 3271
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3
Application US/09721477
INFORMATION:
WT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru

```

Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,477
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of hTERT c
SEQUENCE DESCRIPTION: SEQ ID NO: 343:
US-09-721-477-343

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Query Match 98.5%; Score 3946.6; DB 31; Length 4037
Best Local Similarity 98.9%; Pred. No. 0;
Matches 3992; Conservative 4; Mismatches 3; Indels 36;

[illegible]

09:53:31 2004

UB-09-424-686f-9.rnp

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DB	3481	GACGAGACACCAGCAGCCCTGTCA CGCCGGGCTCTACGTCCCAGGGAGGGAGG	
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DB	3661	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGTCGGCTCC	
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DB	3721	GGGCCAGCTTTTCTTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAG	
QY	3752	CCAGATTGCGCAATTGTTCAACCCCTCGCCCTGCCCTCCTTTGCCCTCCACCCCC	
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DB	4021	AAAAAAAAAAAAA 4035	

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US-09-721-506-343
; Sequence 343, Application US/09721506

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Hailey, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

NUMBER OF SEQUENCES: /2/
CORRESPONDENCE ADDRESS:

CONTEXT ONDENCE ADDRESS: TOWNSEND

ADDRESSEE: IOWINSBRO
STREET: TWO EMPARCA

STREET: TWO EMBALCA
CITY: San Francisco

CITY: SAN FRANCISCO
STATE: CALIFORNIASTATE: California
COUNTRY: USA

COUNTRY: USA
ZIP: 84111-3934

ZIP: 94111-3834
COMPUTER READING FORM

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy
COUNTED ITEMS: 1

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COMPUTER: IBM PC compatible

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OPERATING SYSTEM: P

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FTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION DATA:

PLICATION NUMBER: US/09/721,506

ING DATE: 22-Nov-2000

ASSIFICATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: US 08/724,643

ING DATE: 01-OCT-1996

PLICATION NUMBER: US 08/844,419

ING DATE: 18-APR-1997

PLICATION NUMBER: US 08/846,017

ING DATE: 25-APR-1997

PLICATION NUMBER: US 08/851,843

ING DATE: 06-MAY-1997

PLICATION NUMBER: US 08/854,050

ING DATE: 09-MAY-1997

PLICATION NUMBER: US 08/911,312

ING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/912,951

ING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/915,503

ING DATE: 14-AUG-1997

PLICATION NUMBER: WO PCT/US97/17618

ING DATE: 01-OCT-1997

PLICATION NUMBER: WO PCT/US97/17885

ING DATE: 01-OCT-1997

/AGENT INFORMATION:

4E: Apple, Randolph Ted

ISTRATION NUMBER: 36,429

ERENCE/DOCKET NUMBER: 015389-002610US

UNICATION INFORMATION:

EPHONE: (415) 576-0200

EFAX: (415) 576-0300

FOR SEQ ID NO: 343:

3 CHARACTERISTICS:

NGTH: 4037 base pairs

PE: nucleic acid

RANDEDNESS: single

POLOGY: linear

3 TYPE: cDNA

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4E/KEY: CDS

ATION: 56..3454

ER INFORMATION: /note= "refined sequence of hTERT cDNA"

3 DESCRIPTION: SEQ ID NO: 343:

}

ilarity 98.5%; Score 3946.6; DB 31; Length 4037;
Conservative 4; Mismatches 3; Indels 36; Gaps 1;

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Application US/10325810
INVENTION:
INVENTOR: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
INVENTOR: Human Telomerase Catalytic Subunit
OF SEQUENCES: 633
INVENTOR ADDRESS:
RESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, Eighth Floor
RY: San Francisco
ATE: California
NTRY: USA
P: 94111-3834
R READABLE FORM:
IUM TYPE: Floppy disk
PUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/10/325,810
LING DATE: 20-Dec-2002
ASSIPICATION: <Unknown>
PLICATION DATA:
PLICATION NUMBER: US/09/402,181
LING DATE: 29-Sep-1997
PLICATION NUMBER: US 08/724,643
LING DATE: 01-OCT-1996
PLICATION NUMBER: US 08/844,419
LING DATE: 18-APR-1997
PLICATION NUMBER: US 08/846,017
LING DATE: 25-APR-1997
PLICATION NUMBER: US 08/851,843
LING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
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US-10-325-810-343

Query Match 98.5%; Score 3946.6; DB 49; Length 4037
Best local Similarity 98.9%; Pred. No. 0;
Matches 3992; Conservative 4; Mismatches 3; Indels 36;
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RESULT 10
US-08-974-524E-117
; Sequence 117, Application US/08974524E
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 477
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,524E
; FILING DATE: 19-Nov-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 015389-002950US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:

E CHARACTERISTICS:
NGTH: 4038 base pairs
PE: nucleic acid
RANDEDNESS: single
POLOGY: linear
E TYPE: CDNA
ME/KEY: CDS
CATION: 56..3454
HER INFORMATION: /note= "refined hTERT DNA sequence"
E DESCRIPTION: SEQ ID NO: 117:
17

98.5%; Score 3946.6; DB 13; Length 4038;
ilarity 98.9%; Pred. No. 0;
Conservative 4; Mismatches 3; Indels 36; Gaps 1;
AGCGTGCCTCCTGCTGCGACGTGGGAAGCCCTGGCCCGGCGCCACCCCGCGATGCC 67
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Db 1801 CAAGTTCGAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGTCCGGGA

QY 1868 GGAAGCAGAGTGCAGGAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCAG

Db 1861 GGAAGCAGAGTGCAGGAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCAG

QY 1928 CTTTCATCCCCAAGCCTGACGGGCTGCGGCGGATTTGTGAACATGGACTACGTCGT

us-09-424-686f-9.rnp

98.5%; Score 3946.6; DB 13; Length 4038;
 ilarity 98.9%; Pred. No. 0;
 Conservative 4; Mismatches 3; Indels 36;

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Db	1	GCAGCGCTGCGTCTCTGCTGCGCACGTGGGAAGCCCTGGGCCCGCGCCACACCCCGC
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Db	61	GCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCG
QY	128	GCGCTGGCCACGTTCTGTGGCGCCTTCCGCGCGTGGTGGCCAGTGCCTGGTGTGCGTGCCCT
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QY	188	GGACCCGCGGCTTTCCGCGCGTGGTGGCCAGTGCCTGGTGTGCGTGCCCT
Db	181	GGACCCGCGGCTTTCCGCGCGTGGTGGCCAGTGCCTGGTGTGCGTGCCCT
QY	248	ACGGCGCCCCCGCGCCCTCTTCCGCCAGGTGTCTGCTGCCTGAAGGAGC
Db	241	ACGGCGCCCCCGCGCCCTCTTCCGCCAGGTGTCTGCTGCCTGAAGGAGC
QY	308	CCGAGTGTGACAGGCTGTGCGAGCGCGCGCGGAGAACTGCTGGCCTTCCGCTGAGGAGC
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QY	368	GCTGTGGACGGGGCCCGCGGGGCCCCCGAGGGCTTCAACACAGCGTGC
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QY	428	CCTGCCAAACACGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGC
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QY	488	CCGCTGGGGACGACGTGCTGGTTTCACTGCTGGSACGCTGCGGCTCTTTTG
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QY	548	GGTCCACAGTGCCTTACCAGGTGTGCGGGCGCGCTGTACCAGTCTGGCG
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QY	608	TCAGGCCGGCCCCCGCCACACGCTAGTGACCCCGGAAGCGTCTGGGATGCG
Db	601	TCAGGCCGGCCCCCGCCACACGCTAGTGACCCCGGAAGCGTCTGGGATGCG
QY	668	CTGGAACTATAGCTCAGGAGCGCGGGTCCCCCTGGGCTGCCAGCCCCCG
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QY	728	GAGCGCGGGGCGAGTGCCAGCCGAACTCTGCGCTTGGCCAGAGGCGCAGGC
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QY	788	TGCCCTGAGCCGAGCGGACGCCCGTTGGCAGGGGTCTGGGCCACACCCCG
Db	781	TGCCCTGAGCCGAGCGGACGCCCGTTGGCAGGGGTCTGGGCCACACCCCG
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Db	841	GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCCGCG
QY	908	CACCTCTTTGGAGGTGCGCTCTCTGGCACGCGCCACTCCCAACCATCCGTGG
Db	901	CACCTCTTTGGAGGTGCGCTCTCTGGCACGCGCCACTCCCAACCATCCGTGG
QY	968	GCACCACGGGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCG
Db	961	GCACCACGGGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCG
QY	1028	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGGAGCA
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGGAGCA
QY	1088	GCGCTCTTCTACTACAGCTCTCTGAGGCCAGCCCTGACTGGGCTCGGAGGCT

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us-09-424-686f-9.rnp

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QY	3749	TCCCCAGATTGGCCATTGTTTACCCCTCGCCCTGCCCTCCTTTGGCTTCCACCC
Db	3781	TCCCCAGATTGGCCATTGTTTACCCCTCGCCCTGCCCTCCTTTGGCTTCCACCC
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Db	3841	TCCAGGTGGAGACCCCTGAGAAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACC
QY	3869	GTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCT
Db	3901	GTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCT
QY	3929	GGGAGGTGCTGTGGGAGTAAATACTGAATATATAGATTTTTCAGTTTGAAT
Db	3961	GGGAGGTGCTGTGGGAGTAAATACTGAATATATAGATTTTTCAGTTTGAAT
QY	3989	AAA 3991
Db	4021	AAA 4023
RESULT 13		
US-08-911-312-1		
; Sequence 1, Application US/08911312		
; GENERAL INFORMATION:		
; APPLICANT: Cech, Thomas R.		
; APPLICANT: Lingner, Joachim		
; APPLICANT: Nakamura, Toru		
; APPLICANT: Chapman, Karen B.		
; APPLICANT: Morin, Gregg B.		
; APPLICANT: Harley, Calvin B.		
; APPLICANT: Andrews, William		
; TITLE OF INVENTION: Telomerase Reverse Transcriptase		
; NUMBER OF SEQUENCES: 170		
; CORRESPONDENCE ADDRESS:		
; ADDRESSEE: Townsend and Townsend and Crew LLP		
; STREET: Two Embarcadero Center, Eighth Floor		
; CITY: San Francisco		
; STATE: California		
; COUNTRY: USA		
; ZIP: 94111-3834		
; COMPUTER READABLE FORM:		
; MEDIUM TYPE: Floppy disk		
; COMPUTER: IBM PC compatible		
; OPERATING SYSTEM: PC-DOS/MS-DOS		
; SOFTWARE: PatentIn Release #1.0, Version #1.30		
; CURRENT APPLICATION DATA:		
; APPLICATION NUMBER: US/08/911,312		
; FILING DATE: 14-AUG-1997		
; CLASSIFICATION: 536		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/724,643		
; FILING DATE: 01-OCT-1996		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/844,419		
; FILING DATE: 18-APR-1997		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/846,017		
; FILING DATE: 25-APR-1997		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/851,843		
; FILING DATE: 06-MAY-1997		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/854,050		
; FILING DATE: 09-MAY-1997		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/912,951		
; FILING DATE: 14-AUG-1997		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/915,503		
; FILING DATE: 14-AUG-1997		
; ATTORNEY/AGENT INFORMATION:		
; NAME: Einhorn, Gregory P.		

ION NUMBER: 38,440
/DOCKET NUMBER: 015389-002500US
CATION INFORMATION:
: (415) 576-0200

OR SEQ ID NO: 1:
ARACTERISTICS:
7029 base pairs
cleic acid
ESS: single
linear
PE: cdna

CDS
782..4177
ORMATION: /product= "human telomerase reverse
ORMATION: transcriptase (hTRT)"
ORMATION: /note= "cdna contained in plasmid
ORMATION: pGRN121"

ilarity 98.2%; Score 3933.4; DB 13; Length 7029;
Conservative 99.1%; Pred. No. 0;
Conservative 0; Mismatches 1; Indels 36; Gaps 1;

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QY 726 AGGAGGCGCGGGGCGAGTGCCAGCCGAAAGTCTGCGTTGCCCAAGAGGCCCAGG
Db 1445 AGGAGGCGCGGGGCGAGTGCCAGCCGAAAGTCTGCGTTGCCCAAGAGGCCCAGG
QY 786 GCTGCCCCCTGAGCCGAGCGGACGCCCGCTTGGGAGGGGTCTTGGGCCACCCG
Db 1505 GCTGCCCCCTGAGCCGAGCGGACGCCCGCTTGGGAGGGGTCTTGGGCCACCCG
QY 846 ACGGCTGGACCGAGTGACCGTGGTTTCTGTGTGTGTACCTGCCAGACCCGCG
Db 1565 ACGGCTGGACCGAGTGACCGTGGTTTCTGTGTGTGTACCTGCCAGACCCGCG
QY 906 GCCACCTCTTTGGAGGCTGCGCTCTCTGCGCACGCGCCACTCCCACCCATCCGTC
Db 1625 GCCACCTCTTTGGAGGCTGCGCTCTCTGCGCACGCGCCACTCCCACCCATCCGTC
QY 966 CAGCACCAAGCGGGGCCCCCATCCACATCGCGGCGCACCATGCTCCCTGGGACAG
Db 1685 CAGCACCAAGCGGGGCCCCCATCCACATCGCGGCGCACCATGCTCCCTGGGACAG
QY 1026 CCCCCGCTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGGAG
Db 1745 CCCCCGCTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGGAG
QY 1086 CGGCCCCCTCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGGCGCTCGGAGG
Db 1805 CGGCCCCCTCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGGCGCTCGGAGG
QY 1146 GAGACCATCTTCTGGGTTCCAGGCCCTGATGCGCAGGGACTCCCCCGAGGTTG
Db 1865 GAGACCATCTTCTGGGTTCCAGGCCCTGATGCGCAGGGACTCCCCCGAGGTTG
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QY 1326 GCAGCCGCTGTCTGTGCCCGGGAGAACCCCAAGGCTCTGTGGCGGCCCGCGAG
Db 2045 GCAGCCGCTGTCTGTGCCCGGGAGAACCCCAAGGCTCTGTGGCGGCCCGCGAG
QY 1386 GACACAGACCCCGCTGCTGGTGCAGTGTCTCGGCCAGCACAGACGCCCTGG
Db 2105 GACACAGACCCCGCTGCTGGTGCAGTGTCTCGGCCAGCACAGACGCCCTGG
QY 1446 TACGGCTTCTGTGGGCTGCTGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTG
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QY 1506 CACAAACGACCGCGCTTCTCAGGAACACCAAGAAAGTTTCTCTCCCTGGGGAAG
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2 09:53:31 2004

us-09-424-686f-9.rnppm

Application US/08911312A

INVENTOR:

Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William

INVENTION: Telomerase Reverse Transcriptase

SEQUENCES: 171

INCE ADDRESS:

Two Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
San Francisco
California
USA

11-3834

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patent in Release #1.0, Version #1.30

LICATION DATA:

ON NUMBER: US/08/911,312A

TE: 14-AUG-1997

ATION: 536

CATION DATA:

ON NUMBER: US 08/724,643

TE: 01-OCT-1996

CATION DATA:

ON NUMBER: US 08/844,419

TE: 18-APR-1997

CATION DATA:

ON NUMBER: US 08/846,017

TE: 25-APR-1997

CATION DATA:

ON NUMBER: US 08/851,843

TE: 06-MAY-1997

CATION DATA:

ON NUMBER: US 08/854,050

TE: 09-MAY-1997

CATION DATA:

ON NUMBER: US 08/912,951

TE: 14-AUG-1997

CATION DATA:

ON NUMBER: US 08/915,503

TE: 14-AUG-1997

ENT INFORMATION:

rhorn, Gregory P.

ION NUMBER: 38,440

/DOCKET NUMBER: 015389-002500US

CATION INFORMATION:

: (415) 576-0200

(415) 576-0300

OR SEQ ID NO: 1:

ARACTERISTICS:

7029 base pairs

cleic acid

BSS: single

linear

PE: CDNA

CDS

782..4177

ORMATION: /product= "human telomerase reverse

ORMATION: transcriptase (hTRT)"

ORMATION: /note= "cdna contained in plasmid

ORMATION: pGRN121"

US-08-911-312A-1

Query Match 98.2%; Score 3933.4; DB 13; Length 702;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3980; Conservative 0; Mismatches 1; Indels 36;

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Db	725	ACGACGGCTCGCTCTGCTGGCAGCGTGGGAGCCCTGGCCCGGGCCACCCCG
QY	66	CCGCGCGCTCCCGCTGCCGAGCGCTGCCCTCCCTGCTGGCAGCCACTACCG
Db	785	CCGCGCGCTCCCGCTGCCGAGCGTGGCTCCCTGCTGGCAGCCACTACCG
QY	126	CTGCGCTGGCCACGTTCTGCGCGCGCTGGGGCCCCCAGGCTGGCGGTGGT
Db	845	CTGCGCTGGCCACGTTCTGCGCGCGCTGGGGCCCCCAGGCTGGCGGTGGT
QY	186	GGGACCCCGCGGCTTTCCGCGCGCTGGTGGCCCCAGTGCCTGGTGGTGGCC
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QY	246	GCACGGCGCCCCCGCGCGCTCTCTTCCGCCAGGTGCTCTGCTGAAAGGAG
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QY	306	GCCCCAGTGTGCAGAGGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCTT
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Db	1505	GCTGCGCTGAGCGGAGCGGACCGCGCTTGGGCGAGGGTCTCTGGGCGCCACCCG
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plication PC/TUS0115774

ATTENTION:

is Pharmaceuticals, Inc.

rett P. Monia

William Gaarde

usan M. Freier

Edward V. Wancewicz

NOTATION: ANTISENSE MODULATION OF TERT EXPRESSION

E: ISPH-0568

CATION NUMBER: PCT/US01/15774

G DATE: 2001-05-15

TION NUMBER: 09/572,423

DATE: 2000-05-16

ID NOS: 108

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Matches 3979; Conservative 0; Mismatches 0; Indels 36;

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GenCore version 5.1.6
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cleic search, using sw model

February 29, 2004, 17:50:03 ; Search time 6348.2 Seconds
(without alignments)
18844.394 Million cell updates/sec

US-09-424-686F-9

4006

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IDENTITY_NUC

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length: 0
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Maximum Match 100%
Listing first 45 summaries

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- 27: gb_gss1:*
- 28: gb_gss2:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	ID	Description
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31.3	1584	29	AY407350	AY407350 Pan trogl
21.4	1835	29	AY407351	AY407351 Mus muscu
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ALIGNMENTS

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DEFINITION	AY407349				
ACCESSION	AY407349.1	GI:39763320			
VERSION	AY407349.1	GI:39763320			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
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AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariv Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,E Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J. Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse or gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1826)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariv Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,E Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J. Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

troglodytes TERT gene, VIRTUAL TRANSCRIPT, partial sequence, mic survey sequence.

7350
7350.1 GI:39763321

troglodytes (chimpanzee)

troglodytes

ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; alia; Eutheria; Primates; Catarrhini; Homnidae; Pan. bases 1 to 1584)

k, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 iera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 s, M.D. and Cargill, M.

ring nonneutral evolution from human-chimp-mouse orthologous trios

ence 302 (5652), 1960-1963 (2003)

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bases 1 to 1584)
k, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
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s, M.D. and Cargill, M.

S.M.D. and Cargill, M.
ct Submission

itted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

ville, MD 20850, USA

sequence was made by sequencing genomic exons and ordering based on alignment.

Location/Qualifiers

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ilarity 82.8%; Pred. No. 1.5e-144;

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Conservative	0	Mismatches	236	Indels	36	Gaps	1

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GTGGCTCTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTC 60

CACTGGCTGATGAGTGTGTACGTCTGTCGAGCTGCTCAGGTCCTTCTCTTTATGTCACGG 1755

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[illegible]

GTCAAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCC 193

GTCAGGCAGCATCAGGAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCC 300

1. The first step in the process of creating a new product is to identify a market need. This involves conducting market research to understand what consumers want and what problems they are facing. Once a need is identified, the next step is to develop a concept for a product that addresses that need. This is often done through brainstorming sessions with a team of designers and engineers. The concept is then refined through prototyping and testing, with feedback from potential users being used to make improvements. Once the product is ready for launch, the final step is to create a marketing plan to promote the product and drive sales. This typically involves a combination of digital marketing, social media, and traditional advertising methods. The success of the product will depend on how well it meets the market need and how effectively it is marketed.

AAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCTGTGGAGCCAGAACGT 360

ATCCTGAAAGCCCAAGACGCAG 3183
|||||
ATCCTGAAAGCCCAAGACGCAG 1584

7351 1835 bp DNA linear GSS 15-DEC-2003
musculus TERT gene, VIRTUAL TRANSCRIPT, partial sequence,
nic survey sequence.
7351
7351.1 GI:39763322

musculus (house mouse)
musculus
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Mus musculus
Mus musculus, S., Nielson, R., Thomas, P., Kejariwal, A.,
Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
M.D. and Cargill, M.
Orthologous evolution from human-chimp-mouse orthologous
trios

1302 (5652), 1960-1963 (2003)
Mus musculus
Mus musculus, S., Nielson, R., Thomas, P., Kejariwal, A.,
Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
M.D. and Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Baltimore, MD 20850, USA
Sequence was made by sequencing genomic exons and ordering
based on alignment.

Location/Qualifiers
1.1835
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1835
/gene="TERT"
/locus_tag="HCM2861"

21.4%; Score 858.4; DB 29; Length 1835;
Identity 64.4%; Pred. No. 5.2e-96;
Conservative 0; Mismatches 609; Indels 45; Gaps 4;
TTGGCTGTTCGGCCGCGAGACCGCTCTCGGTGAGGAGATCTTGGCCAAAGTTCC 1695
AGGACCGTGTCCCGCTGCAGAGACCGCTCTGAGGAGAGAGATCTTGGCTACGTTCC 60
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACGG 1755
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACAG 120
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACAG 1815
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACAG 1875
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACAG 240
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACAG 1935
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACAG 300
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACAG 1995
TCTGGCTGATGAGTGTGTACGTCTCGGTGAGTGTCTCAGGTCTTTCTTTATGTCACAG 360

GATCCTCCTGCTGACGGGTACAGGTTTACGCATGTGTGCTGACGCTCCCATTTTCAT 3092
|||||
GATCTTCTGCTTACGGCTTACAGGTTTCCATGTCATGTGTGATTCAGCTTCCCTTTGAC 1500
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GCAAGTTTGAAGAAGCCCAACATTTTCTGCGCGTTCATCTGTGACAGGCTCCCTC 3152
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CTACTCCATCCTGAAAGCCCAAGACGACGGGATGTGCTGG--GGGCCAAGGGCGCG 3210
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CTATGCTATCCTGAAGGTCAAGATCCAGTGATCCCCCAGGAATGACACTAAAGGCT 1620
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ACTCGACACGCTGTACCTACGTGCTCACTCCTGGGTCACTCAGGACAGCCCAAGCGC 3330
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GCTGCTCATCTGTATCAAAATGTCTCCTGGGACCTCTGAGGACAGCCCCAAAAC 1740
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CTGAGTGGGAAGCTCCCGGACGACGCTGACTGCTCCTGAGGCGCGCAGCAACCGG 3390
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CTGTGCGGAAGCTCCAGAGGCGACAATGACCATCTTAAAGCTGCAGTGAACCCAG 1800
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3198 925 bp mRNA linear EST 05-FEB-2002
COURT_6387556 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840
mRNA sequence.

3198
3198.1 GI:18502238

sapiens (human)
sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 925
MGC <http://mgi.nci.nih.gov/>.
onal Institutes of Health, Mammalian Gene Collection (MGC)
lished (1999)
act: Robert Strausberg, Ph.D.
l: cgapbs-r@mail.nih.gov
e Procurement: ATCC
A Library Preparation: Life Technologies, Inc.
A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Agencourt Bioscience Corporation
e distribution: MGC clone distribution information can be
d through the I.M.A.G.E. Consortium/LLNL at:
://image.llnl.gov
3: LLAM12208 row: p column: 01
quality sequence stop: 646.
Location/Qualifiers
1..925
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5529840"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

18.5%; Score 743; DB 12; Length 925;
ilarity 99.1%; Pred. No. 8.6e-82;
Conservative 0; Mismatches 5; Indels 2; Gaps 1;

2183 CATCCCCCAGGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAI
|||||
65 CATTTCCAGGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAI
|||||
2243 CTGCGTGCCTGCGTATGCGTGTCCAGAAAGCCCGCCATGGGACGTCGGCAI
|||||
125 CTGCGTGCCTGCGTATGCGTGTCCAGAAAGCCCGCCATGGGACGTCGGCAI
|||||
2303 CAAGAGCCACGCTCTCTACCTTACAGACCTCCAGCCGTACATCGGACAGTTGAI
|||||
185 CAAGAGCCACGCTCTCTACCTTACAGACCTCCAGCCGTACATCGGACAGTTGAI
|||||
2363 CCTGAGGAGACAGCCCGCTGAGGATGCCGTGTCATCGAGCAGAGCTCCTC
|||||
245 CCTGAGGAGACAGCCCGCTGAGGATGCCGTGTCATCGAGCAGAGCTCCTC
|||||
2423 TGAGGCCAGCAGTGGCTCTTTCGACGTCTTCTACGTTTCATGTGCCACCGAI
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305 TGAGGCCAGCAGTGGCTCTTTCGACGTCTTCTACGTTTCATGTGCCACCGAI
|||||
2483 CATCAGGGGCAAGTCTTACGTCCAGTCCAGGGATCCCGCAGGGCTCCATCCTI
|||||
365 CATCAGGGGCAAGTCTTACGTCCAGTCCAGGGATCCCGCAGGGCTCCATCCTI
|||||
2543 GCTGCTCTGCAGCCTGTGTACGGGACATGGAGAACAAAGCTGTTTGGGGGAI
|||||
425 GCTGCTCTGCAGCCTGTGTACGGGACATGGAGAACAAAGCTGTTTGGGGGAI
|||||
2603 GGACGGGCTGCTCCTGCTTGGTGGATGATTTCTTGTGGTACACCTCACCTI
|||||
485 GGACGGGCTGCTCCTGCTTGGTGGATGATTTCTTGTGGTACACCTCACCTI
|||||
2663 CGCGAAACCTTCTCCTCAGGACCTGTCGAGGTCCTGAGTATGGTGGCTGCTI
|||||
545 CGCGAAACCTTCTCCTCAGGACCTGTCGAGGTCCTGAGTATGGTGGCTGCTI
|||||
2723 CTTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGC
|||||
605 CTTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGC
|||||
2783 TGTTCAGATGCCGGCCACGGCCTATTCCCTGTGTGGGCTGCTGTGGATAC
|||||
665 TGTTCAGATGCCGGCCACGGCCTATTCCCTGTGTGGGCTGCTGTGGATAC
|||||
2843 CTTGAGGTGCAGAGCGGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAG
|||||
725 CTTGAGGTGCAGAGCGGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAG
|||||
2903 CTTCAACCGCGGCTTCAA--GGCTGGGAGGAACATGCGTGGCAA 2945
|||||
785 CTTCAACCGCGGCTTCAAAGGCTGGGAAGGAACATGCGTGGCAA 829
|||||

RESULT 5
BU702370
LOCUS
DEFINITION
UI-M-F10-byx-f-12-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA
IMAGE:6400523 5', mRNA sequence.
BU702370
BU702370.1 GI:23627105
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
1 (bases 1 to 851)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa


```
ilarity 99.6%; Pred. No. 1.1e-47;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CCCAGGCCGACACCGCTGGAGTCTGAGGCTGAGTGGCCGAGGCTGCA 3573
|||||
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TCCGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGTGGCCGAGGCTGA 3633
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GTCAGCACACCTGCCGCTTCACTTCCCCACAGGCTGGGCTCCACCCGAG 3693
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GTCAGCACACCTGCCGCTTCACTTCCACAGGCTGGGCTCCACCCGAG 289
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CAGCTTTTCTCACCAGGAGCCCGCTTCACTTCCACATAGGAATAGTCCATCCC 3753
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CAGCTTTTCTCACCAGGAGCCCGCTTCACTTCCACATAGGAATAGTCCATCCC 229
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ATTCGCCATTGTTACCCCTCGCCCTGCCCTTCCCTTGGCTTCCACCCATCCAG 3813
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GGAGACCCCTGAGAGGACCCCTGGAGCTCTGGAAATTTGGAGTGACCAAGGTGTC 3873
|||||
GGAGACCCCTGAGAGGACCCCTGGAGCTCTGGAAATTTGGAGTGACCAAGGTGTC 109
|||||
GTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTTGGGTCAAATTTGGGGGA 3933
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GTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTTGGGTCAAATTTGGGGGA 49
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4748 492 bp mRNA linear EST 06-MAR-2002
T0096335 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-99-E07
mRNA sequence.
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4748
4748.1 GI:19181161
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sapiens (human)
sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 492)
.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Y.S.
Frontier Korean EST Project 2001
lished (2002)
act: Kim YS
ne Research Center
a Research Institute of Bioscience & Biotechnology
Jeon-dong Yuseong-gu, Daejeon 305-333, South Korea
+82-42-860-4470
+82-42-860-4409
l: yongsung@mail.kribb.re.kr
a: 99 row: E column: 07
quality sequence stop: 492.
Location/Qualifiers
1. .492
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/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
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/lab_host="DH10B"
/clone_lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site
Site_2: NotI; The S22SNU16 library was contri-
Soares laboratory and it was constructed as de
Bonardo, M.F., Lennon, G. and Soares, M.B. (19
Research 6(9): 791-806. RNA was prepared from
cells of SNU-16 culture. SNU-16 cell was obtai
Korean Cell Line Bank (KCLB). SNU-16 was establ
ascitic fluids of Korean patients by Park J.G.
(1990), Cancer Res 50: 2773-2780."
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ORIGIN

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Query Match 11.1%; Score 445; DB 12; Length 492;
Best Local Similarity 100.0%; Pred. No. 3.4e-45;
Matches 445; Conservative 0; Mismatches 0; Indels 0;
QY 2739 GTGAACCTCCCTGTAGAGACGAGGCCCTGGTGCGACGGCTTTGTTTCAGATC
Db 1 GTGAACCTCCCTGTAGAGACGAGGCCCTGGTGCGACGGCTTTGTTTCAGATC
QY 2799 CACGGCCCTATTCCCTGTGGTGGCCCTGCTGCTGGATACCCGACCCCTGGAGGT
Db 61 CACGGCCCTATTCCCTGTGGTGGCCCTGCTGCTGGATACCCGACCCCTGGAGGT
QY 2859 GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCCG
Db 121 GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCCG
QY 2919 AAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGCTTTGCGGCTGAAAGTG
Db 181 AAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGCTTTGCGGCTGAAAGTG
QY 2979 CTGTTTCTGGATTTCAGAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTAC
Db 241 CTGTTTCTGGATTTCAGAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTAC
QY 3039 CTCCTGCTGACGGCGTACAGGTTTTCAGCATGTGCTGCAGCTCCCATTTTCAI
Db 301 CTCCTGCTGACGGCGTACAGGTTTTCAGCATGTGCTGCAGCTCCCATTTTCAI
QY 3099 GTTTGGAAGAACCCCACTTTTCTGCGCGTCACTCTTGACACGGCCTCCCTC
Db 361 GTTTGGAAGAACCCCACTTTTCTGCGCGTCACTCTTGACACGGCCTCCCTC
QY 3159 TCCATCCTGAAAGCCCAAGAACGCAG 3183
Db 421 TCCATCCTGAAAGCCCAAGAACGCAG 445
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RESULT 8

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LOCUS BG917907
DEFINITION BG917907 851 bp mRNA linear EST
602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:
mRNA sequence.
ACCESSION BG917907
VERSION BG917907.1 GI:14298383
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
1 (bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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1296 389 bp mRNA linear EST 14-AUG-1997
g02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',
sequence.
1296
1296.1 GI:1924194
sapiens (human)
sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 389)
CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
r Gene Index
blished (1997)
act: Robert Strausberg, Ph.D.
l: cgapbs-r@mail.nih.gov
clone is available royalty-free through LLNL; contact the
E Consortium (info@image.llnl.gov) for further information.
rt Length: 2187 Std Error: 0.00
primer: -28ml3 rev2 ET from Amersham
quality sequence stop: 385.
Location/Qualifiers
1. 389
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/clone_lib="NCI CGAP GCB1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGCGCTCATTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

9.6%; Score 385.8; DB 9; Length 389;
ilarity 99.5%; Pred. No. 6.6e-38;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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TGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 1805
|||||
TGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 120
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QY 1806 AGCAAGTTGCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGTGC GG
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Db 121 AGCAAGTTGCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGTGC GG
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QY 1866 TCGGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTC C
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Db 181 TCGGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTC C
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QY 1926 CGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGACTACGTC
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Db 241 CGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGACTACGTC
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QY 1986 GCCAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCTCTCACCTCGAGGGTGAAC
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Db 301 GCCAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCTCTCACCTCGAGGGTGAAC
|||||
QY 2046 TTCAGCGTCTCAACTACGAGCGGGCGG 2074
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Db 361 TTCAGCGTCTCAACTACGAGCGGGCGG 389
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RESULT 11
CF531121
LOCUS
DEFINITION
CF531121
IMAGE:30355988 5', mRNA sequence.
ACCESSION
CF531121
VERSION
CF531121.1 GI:34583085
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
1 (bases 1 to 688)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Universi
CDNA Library Arrayed by: Dr. M. Bento Soares, Universit
DNA Sequencing by: Dr. M. Bento Soares, University of I
Clone Distribution: Distribution information can be fou
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anato
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. 688
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/db_xref="taxon:10090"
/clone="IMAGE:30355988"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP FY0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1:
Site 2: Not I; The library was constructed acco
Bonaldo, Lennon and Soares, Genome Research, 6:
1996. Denatured RNA was size fractionated on a
gel. First strand cDNA synthesis was primed wit
primer containing a Not I site. Double strand c
size selected according to mRNA size fraction,
with EcoR I adaptor, digested with NotI and the
directionally into pYX-Asc vector. The library
sequence located between the Not I site and the
is AGCGAGACAG. This library was created for the
Iowa Brain Anatomy Project (BMAP): 'Gene Discov
Developing Mouse Nervous System', supported by I
Institute of Mental Health (NIMH), Hemin Chin,

program coordinator."

8.6%; Score 346.2; DB 14; Length 688;
ilarity 73.9%; Pred. No. 4e-33;
Conservative 0; Mismatches 155; Indels 0; Gaps 0;
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|||||
CGGCTTGAGCACAAATGACCGCGGCTCCTGTTGCCCCGGGTGCGCTCTCTGCTGCG 122
|||||
3CCACTACCGGAGGTGCTGCCGCTGGCCACGTTCTGCGGCGCTTGGGGCCCCAGGG 166
|||||
3CCGATACCGGAGGTGTCGCGCTGGCAACCTTTGTCGCGCGCTGGGGCCCCAGGG 182
|||||
3CGGCTGTTGTCAGCGCGGGACCCGCGGCTTTCCGCGCGCTGTTGGCCAGTGCCT 226
|||||
3CGGCTTGTGCAACCCGCGGACCCGAAGATCTACCGCACTTTGTTGCCCAATGCCT 242
|||||
TGTCGCTGCCCTGGGACGACCGCGCGCCCGCCCGCGCTTCCCTTCCGCGAGGTGC 286
|||||
TGTCATGCACTGGGCTCACAGCCTCCACCTGCGGACCTTTCTTCCACAGGTGC 302
|||||
3CCTGAAGGAGCTGTTGCGCCGAGTGTCTGCAGAGGCTGTGCGAGCGCGCGGAAGAA 346
|||||
CCCTGAAGAGCTGTTGCGCAGGTTGTGCAGAGACTCTGCGAGCGCAACAGAGAAA 362
|||||
TGCTGGCCTTCGGCTTCGGCTGCTGGACGGGGCGCGGGGGCCCCCGCGAGGCCTT 406
|||||
TGCTGGCTTTTGGCTTTGAGCTGCTTAACAGAGCGAGGCGGGCTCCCATGGCCTT 422
|||||
2CACCAGCTGCGAGTACCTGCCCAACACGGTGACCGACGCTGCGGGGAGCGG 466
|||||
TAGTAGCTGCGTAGTACTTGCCCAACACTGTTATTGAGACCCCTGCGTCTCAGTGG 482
|||||
TGTTGGGCTGCTGCTGCGCGCGGTGGCGGACGAGCTGCTGTTTACCTGCTGGCACG 526
|||||
TAGTATGCTACTGTTAGCGGAGTGGCGGACGACCTGCTGTTACCTGCTGGCACA 542
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3CGCGCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586
|||||
TGCTCTTTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
|||||
ACCAGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
|||||
TAAACCCCTCATCTCTACTCAGCANCCTCCAGCCTAACTTGAAGTGGGGCC 655
|||||

1069 649 bp mRNA linear EST 12-SEP-2003
-FY0-cgp-c-19-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
3:30355746 5', mRNA sequence.
1069
1069.1 GI:34583033
musculus (house mouse)
musculus
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ases 1 to 649)
AGC <http://mgc.nci.nih.gov/>.
nal Institutes of Health, Mammalian Gene Collection (MGC)
lished (1999)
act: Robert Strausberg, Ph.D.
l: cgapbs-remail.nih.gov
e Procurement: Dr. Jim Lin, University of Iowa
a Library preparation: Dr. M. Bento Soares, University of Iowa
a Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Sequencing by: Dr. M. Bento Soares, University of Iowa
e Distribution: Distribution information can be found at
://genome.uiowa.edu/distribution/mousefl.html
3 clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. .649
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355746"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1:
Site 2: Not I; The library was constructed acco
Bonaldo, Lennon and Soares, Genome Research, 6:
1996. Denatured RNA was size fractionated on a
gel. First strand cDNA synthesis was primed wit
primer containing a Not I site. Double strand c
size selected according to mRNA size fraction, c
with EcoR I adaptor, digested with NotI and the
directionally into pYX-Asc vector. The library
sequence located between the Not I site and the
is AGCGAGACAG. This library was created for the
Iowa Brain Anatomy Project (BMAP): 'Gene Discov
Developing Mouse Nervous System', supported by
Institute of Mental Health (NIMH), Hemin Chin,
program coordinator."

ORIGIN

Query Match 8.5%; Score 340.4; DB 14; Length 649;
Best Local Similarity 77.3%; Pred. No. 2.1e-32;
Matches 413; Conservative 0; Mismatches 121; Indels 0;
QY 47 CCCGGCCACCCCGCGATGCCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCT
|||||
Db 26 CCCGGCCTTGAGCACAAATGACCCGCGCTCTCGTTGCCCGCGGTGCGCTCT
|||||
QY 107 CAGCCACTACCGGAGGTGTCGCGCTGGGCACGTTCTGTCGGCGCTGGGGCC
|||||
Db 86 CAGCCGATACCGGAGGTGTGGCGCTGGCAACCTTTGTGCGCGCTGGGGCC
|||||
QY 167 CTGGCGCTGCTGTCAGCGCGGGACCCGCGGCTTCCGCGGCTGCTGGGCGCA
|||||
Db 146 CAGCGGCTTGTGCAACCCGCGGACCCGAGATCTACCGCACTTTGTTGCCCA
|||||
QY 227 GGTGTGCTGCTGCTGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
|||||
Db 206 AGTGTGCTGCTGCTGGGCTCACAGCCTCCACCTGCGGACCTTCTCCACCA
|||||
QY 287 CTGCTGAAGAGCTGTTGGCCCGAGTCTGTCAGAGGCTGTGCGAGCGCGCGCG
|||||
Db 266 ATCCCTGAAGAGCTGTTGGCCAGGTTGTGCAAGACTCTGCGAGCGCAACGA
|||||
QY 347 CGTGTGCGCTTGGCTTGGCTTTGAGCTGCTTAACGAGGCCAGAGCGGCGCTCCCAT
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|||||
QY 407 CACCACAGCGTGGCAGCTACCTGCCCAACACGGTGACCGGACTGCGGCGG
|||||
Db 386 CACTAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
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QY 467 GCGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
|||||
Db 446 TGCTGATGCTACTGTTGAGCGGAGTGGGCGGACGACCTGCTGCTACCTGCT
|||||
QY 527 CTGCGGCTCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
|||||
Db 506 CTGTGCTCTTTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

RESULT 13
BB618671

Sequencing by: National Institutes of Health Intramural
 sequencing Center (NISC)
 Gene distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 @image.llnl.gov
 @1845958
 @: LLAM12043 row: N column: 7
 primer: Sp6 primer.
 Location/Qualifiers
 1. .664
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:5409222"
 /tissue_type="embryo, late gastrula"
 /dev_stage="embryo, 7.5 dpc"
 /lab_host="XL1-Blue"
 /clone_lib="Baker mouse embryo e7.5"
 /note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA
 made by oligo-dT priming. Directionally cloned into
 SalI/NotI sites using the following 5' adaptor:
 5'-TCGACCCACGGCTCCG-3'. Size-selected for average insert
 size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
 University)."

[illegible]

Db 564 ATACGTGGTACAGCTGCTTAGGTCAATCTTTTACATCACAGAGAGACATTCCA

QY 1775 CAGGCTCTTTTTTCTACGGAAGAGTGTCTGGAGCAAGTTGC 1815

Db 624 CAGGCTCTTCTTCTACGTAAGAGTGTGTGGAGCAAGCTGC 664

[illegible]

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Pa
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequenc
 Clone distribution: NCI-CGAP clone distribution informa
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
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 Seq primer: -40ml3 fwd. ET from Amerisham
 High quality sequence stop: 331.

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FEATURES
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1319048"
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            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_GCB1"
            /note="Vector: pT7T3D-Pac (Pharmacia) with a multiple
            linker; Site 1: Not I; Site 2: Eco RI; 1st
            was prepared from human tonsillar cells enriched
            germinal center B cells by flow sorting (CD20+,
            provided by Dr. Louis M. Staudt (NCI), Dr. David
            (NCI) and Dr. Gerald Marti (CBER). cDNA synthesized
            primed with a Not I - oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGCGCTCATTTTTTTTTT
            ]. Double-stranded cDNA was ligated to Eco RI
            (Pharmacia), digested with Not I and cloned into
            and Eco RI sites of the modified pT7T3 vector.
            went through one round of normalization, and was
            constructed by Bento Soares and M. Fatima Bonal

```

ORIGIN	Query Match	7.9%	Score 316.4;	DB 9;	Length 340;
	Best Local Similarity	99.1%;	Pred. No. 2.2e-29;		
	Matches 339;	Conservative 0;	Mismatches 1;	Indels 2;	
Qy	3656	TCAC	TTCCCCC	CAGGCTGGCGCTCGGCTCCAC	CCCCCAGGSCAGCTTTTCTCTCAC(
Dd	340	TCAC	TTCCCCC	CAGG-TGGCGCTCGGCTCCAC	CCCCCAGGSCAGCTTTTCTCTCAC(
Qy	3716	CCCGGCTTCCACTCC	CCCCACATAGGAATAGTCCAT	CCCCCAGATTGCGCAATTGTTCT/	
Dd	281	CCCGGCTTCCACTCC	CCCCACATAGGAATAGTCCAT	CCCCCAGATTGCGCAATTGTTCT/	

2 09:53:32 2004

us-09-424-686f-9.rst

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|||||
CCCTGCCCTCCTTTGCTTCCACCCCAACCATCCAGGTGGAGACCTGAGAAGGACCC 162
|||||
GGAGCTCTGGGAATTTGGAGTGACCAAAAGGTGTGCCCTGTACACAGGCGAGGACCCCTG 3895
|||||
GGAGCTCTGGGAATTTGGAGTGACCAAAAGGTGTGCCCTGTACACAGGCGAGGACCCCTG 102
|||||
CCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAATACT 3955
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CCTGGATGGGGT-CCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAATACT 43
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ATATATGAGTTTTTCAGTTTTTGAAAAA 3997
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ATATATGAGTTTTTCAGTTTTTGAAAAA 1
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: March 1, 2004, 03:42:07
95 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

February 29, 2004, 21:01:14 ; Search time 58.8307 Seconds
(without alignments)
11471.157 Million cell updates/sec

US-09-424-686F-9
4006
1 gtttcaggcagcgtgcgtc.....aaaaaaaaaaaaaaaaaaaa 4006

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

164199 seqs, 84230614 residues

hits satisfying chosen parameters: 328398

length: 0
length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Pending Patents NA New.*
- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
 - 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
 - 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
 - 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
 - 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
 - 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
 - 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB	ID	Description
1.5	1215	6	US-10-767-701-8767	Sequence 8767, Ap
1.5	658	6	US-10-767-701-4204	Sequence 4204, Ap
1.4	637	6	US-10-767-701-25070	Sequence 25070, A
1.4	574	6	US-10-767-701-253	Sequence 253, App
1.4	40000	6	US-10-767-471-10913	Sequence 10913, A
1.4	666	6	US-10-767-701-4866	Sequence 4866, Ap
1.4	584	6	US-10-767-701-4186	Sequence 4186, Ap
1.3	570	6	US-10-767-701-2473	Sequence 2473, Ap
1.3	580	6	US-10-767-701-4466	Sequence 4466, Ap
1.3	1092	6	US-10-767-701-9739	Sequence 9739, Ap
1.3	522	6	US-10-767-701-30024	Sequence 30024, A
1.3	667	6	US-10-767-701-8805	Sequence 8805, Ap
1.3	697	6	US-10-767-701-4420	Sequence 4420, Ap
1.3	14800	6	US-10-767-471-195	Sequence 195, App
1.3	11409	6	US-10-767-471-603	Sequence 603, App
1.3	14321	6	US-10-767-471-191	Sequence 191, App
1.3	14641	6	US-10-767-471-193	Sequence 193, App
1.3	14760	6	US-10-767-471-192	Sequence 192, App
1.3	24841	6	US-10-767-471-10753	Sequence 10753, A
1.3	72779	6	US-10-767-471-10639	Sequence 10639, A
1.3	963	6	US-10-767-701-1482	Sequence 1482, Ap
1.3	667	6	US-10-767-701-4633	Sequence 4633, Ap
1.3	1165	6	US-10-767-701-12235	Sequence 12235, A
1.3	570	6	US-10-767-701-2473	Sequence 2473, Ap
1.3	558	6	US-10-767-701-23530	Sequence 23530, A
1.3	571	6	US-10-767-701-18773	Sequence 18773, A

C	27	50.6	1.3	752	6	US-10-767-701-11390	Sequenc
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	29	50.4	1.3	584	6	US-10-767-701-11623	Sequenc
	30	50.4	1.3	1854	6	US-10-767-701-14885	Sequenc
	31	50	1.2	1126	6	US-10-767-701-13291	Sequenc
C	32	49.8	1.2	658	6	US-10-767-701-4204	Sequenc
	33	49.6	1.2	659	6	US-10-767-701-4135	Sequenc
	34	49.6	1.2	659	6	US-10-767-701-20222	Sequenc
	35	49.6	1.2	4142	6	US-10-601-807-5	Sequenc
	36	49.4	1.2	459	6	US-10-767-701-1801	Sequenc
	37	49	1.2	589	6	US-10-767-701-28671	Sequenc
C	38	49	1.2	1388	6	US-10-767-701-14298	Sequenc
	39	49	1.2	166020	6	US-10-767-471-10806	Sequenc
C	40	48.6	1.2	1215	6	US-10-767-701-8767	Sequenc
C	41	48.4	1.2	666	6	US-10-767-701-4866	Sequenc
C	42	48.2	1.2	615	6	US-10-767-701-4396	Sequenc
	43	48.2	1.2	690	6	US-10-767-701-4070	Sequenc
	44	48.2	1.2	1564	6	US-10-765-790-142	Sequenc
C	45	48.2	1.2	1725	1	PCT-IL03-01008-5	Sequenc

ALIGNMENTS

RESULT 1
US-10-767-701-8767
; Sequence 8767, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules At
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improveme
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8767
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56207_1
US-10-767-701-8767

Query Match	1.5%	Score	60.6;	DB	6;	Length	1215;
Best Local Similarity	49.1%;	Pred. No.	0.00022;				
Matches	188;	Conservative	0;	Mismatches	194;	Indels	1;
QY	28	GCACGTGGGAAGCCCTGGCCCGCCCGCCACCCCGCGATGCGCGCGTCCCGCGT					
Db	1	GCACGAGGACCTTGACGCTCCCGCCATCCCGCGCGCCACCCCTCTCTCCCCC					
QY	88	CCGTGCGTCCCTGCTGCGCAGCCACTACCGCGAGTGTGCTGCCGTCGCCACGI					
Db	61	CCCCCCCCCCCCCGGCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCG					
QY	148	GGCGCTGGGGCCCCCAGGGTGGCGGTGGTGAGCGCGGGGACCGCGGGGCTT					
Db	121	GCCCCCGCCCCCCCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCG					
QY	208	CGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGAAGAGAGTGGTGGCCGAGTGTG					
Db	181	CGCGCGCGCCCTCTGTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG					
QY	268	CCTCTTCCCGCAGTGTCTGCTGAGAGAGTGGTGGCCCGAGTGTGCTGAGAG					
Db	241	CCGCTTCCCGCGCGGACCGCGGAGCGCGCGACGTGCGGGGGGGGGGAGG					
QY	328	GCGAGCGCGCGCGAAGAACGTGCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT					
Db	301	CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG					

valic, David K.
hou, Yihua
ao, Yongwei
NTION: Nucleic Acid Molecules and Other Molecules Associated With
NTION: Plants and Uses Thereof For Plant Improvement
E: 38-21(53535)B
CATION NUMBER: US/10/767,701
G DATE: 2004-01-29
ID NOS: 63128

rgum bicolor

ATION: Clone ID: SORBI-28MAY03-CLUS73536_1
86

1.4%; Score 54.2; DB 6; Length 584;
ilarity 45.7%; Pred. No. 0.0039;
Conservative 0; Mismatches 223; Indels 0; Gaps 0;

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GCGCCCCGCCCCCCCCCTGCCCCCCCCCGCTCTCCCCCCCCCGCCCCCGGCTCGC 263

TCGTGCGGCGCTGGGGCCCCAGGGCTGGCGGTGTGAGCGCGGAGCCCGCGGC 199
CGGCGCGCGCGCGGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 323

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TCCCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 443

GGTGTGCGAGCGCGCGCGGAGAACGTGCTGCGCTTCCGCTTCCGCTTCCGCTTCC 379
GCCAGGCGTCCACTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 503

CCCGCGGGGCCCCCGCGCGCTTACCCAGCGGTGCGCGAGTACCT 430
ACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 554

73/c
Application US/10767701

ATION:
valic, David K.
hou, Yihua
ao, Yongwei
NTION: Nucleic Acid Molecules and Other Molecules Associated With
NTION: Plants and Uses Thereof For Plant Improvement
E: 38-21(53535)B
CATION NUMBER: US/10/767,701
G DATE: 2004-01-29
ID NOS: 63128

rgum bicolor

sure
)..(570)
ATION: unsure at all n locations

ATION: Clone ID: SORBI-28MAY03-CLUS41826_1

US-10-767-701-2473

Query Match 1.3%; Score 53.4; DB 6; Length 570;
Best Local Similarity 52.9%; Pred. No. 0.0058;
Matches 137; Conservative 0; Mismatches 121; Indels 1;

QY 574 GCGGCGCGCGCTGTACAGCTCGGCGTGCCTGCTGCTGCTGCTGCTGCTGCTG 574
Db 260 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 260

QY 634 GTG-GACCCCGAAGCGTCTGGGATGCGAACCGGCTGGAACCATAGCGTCAGC 634
Db 200 GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 200

QY 693 GGGGTCCCCCTGCGCTGCGAGCCCGCGGTGCGAGAGGCGCGGGGCGAGTGCC 693
Db 140 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 140

QY 753 AGTCTGCGGTGCTGCGAGCGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 753
Db 80 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 80

QY 813 GTTGGCAGGGTCTCTGGG 831
Db 20 CGGGGCGCGCGCGCGCGCGG 2

RESULT 9

US-10-767-701-4466
; Sequence 4466, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules As
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvemen
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4466
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS80039_1
US-10-767-701-4466

Query Match 1.3%; Score 53.4; DB 6; Length 580;
Best Local Similarity 52.3%; Pred. No. 0.0058;
Matches 147; Conservative 0; Mismatches 126; Indels 8;

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Db 125 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 125

QY 72 GCTCCCCGCTGCGAGCGCTGCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 72
Db 185 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 185

QY 132 CTGGCCACGTGCTGCGCGCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132
Db 245 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 245

QY 192 CCGCGCGCTTTCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
Db 305 CCTGCTCTCT-----GCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCG 305

QY 252 CCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 252
Db 357 CTCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 357

09:53:31 2004

US-09-424-686f-9.rnpn

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 AGGC--CCGGCCCCCGCCACACGCTAGTAGGACCCCGAAGGCGTCTGGGATCGGAACGG 665
 |||||-----|||||----|||----|||----|||----|||----|||----||
 AGCGGGCGGCGCTCTCTCGGCCAGCTCGCGAACCGGCCGGGCTCGGCCTCCAGCCTCT 5492
 CTGGAACCATAGCGTCAAGGAGCGCGGGGTCCCCCTGGGCGTGCC 712
 |||||----|||----|||----|||----|||----|||----|||----|||----|||
 TTGGACTTCTCGCTGGTGGAGCGGACTCTCTCTCAGCCCTGCCC 5445

3/c
Application US/10767471
ATTORNEY: RIGILL, Michele et al.
INVENTOR: GENETIC POLYMORPHISMS ASSOCIATED WITH
DISEASE: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
E: CL001505
CATION NUMBER: US/10/767,471
F DATE: 2004-01-30
ID NOS: 50231
tSEQ for Windows Version 4.0

no sapiens
3

1.3%; Score 52; DB 6; Length 11409;
 ilarity 44.2%; Pred. No. 0.036;
 Conservative 6; Mismatches 226; Indels 0; Gaps 0;

[illegible]

196
 1764
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GenCore version 5.1.6
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Minimum Match 0%
Maximum Match 100%
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Published Applications NA:*

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ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

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98.2	4015	9	US-09-990-080-1	Sequence 1, Appli
98.2	4015	9	US-09-843-676-224	Sequence 224, App
98.2	4015	9	US-09-953-052-1	Sequence 1, Appli
98.2	4015	14	US-10-053-758-224	Sequence 224, App
98.2	4015	14	US-10-208-243-1	Sequence 1, Appli
98.2	4015	14	US-10-054-295-224	Sequence 224, App
98.2	4015	14	US-10-054-611-224	Sequence 224, App
98.2	4015	14	US-10-105-963-1	Sequence 1, Appli
98.2	4015	14	US-10-044-692-1	Sequence 1, Appli
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ALIGNMENTS

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; Sequence 3, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-733-294A-3

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Matches 3979; Conservative 0; Mismatches 0; Indels 36;

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RESULT 2

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; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
US-09-990-080-1

Query Match 98.2%; Score 3933; DB 9; Length 4015;
Best local Similarity 99.1%; Pred. No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36;

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RESULT 3

US-09-843-676-224

; Sequence 224, Application US/09843676

; Patent No. US20020164786A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. US20020164786A1el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION DATA:
PLING DATE: 26-Apr-2001
ASSIFICATION: 536
APPLICATION DATA:
PLING DATE: 09-MAY-1997
PLING DATE: 25-APR-1997
PLING DATE: 18-APR-1997
PLING DATE: 01-OCT-1996
Y/AGENT INFORMATION:
ME: Apple, Randolph T.
GISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
MUNICATON INFORMATION:
LEPHONE: (415) 576-0200
LEFAX: (415) 576-0300
FOR SEQ ID NO: 224:
E CHARACTERISTICS:
NGTH: 4015 base pairs
PE: nucleic acid
RANDEDNESS: single
POLOGY: linear
E TYPE: CDNA
ME/KEY: CDS
CATON: 56.3454
HER INFORMATION: /product= "hTRT"
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E DESCRIPTION: SEQ ID NO: 224:
4

98.2%; Score 3933; DB 9; Length 4015;
ilarity 99.1%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 36; Gaps 1;
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RMATION:

NT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

F INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase

OF SEQUENCES: 72

ONDENSE ADDRESS:

DRESSEE: Townsend and Townsend and Crew LLP

REET: Two Embarcadero Center, Eighth Floor

TV: San Francisco

ATE: California

UNTRY: USA

P: 94111-3834

R READABLE FORM:

DIUM TYPE: Floppy disk

MPUTER: IBM PC compatible

ERATING SYSTEM: PC-DOS/MS-DOS

FTWARE: Patentin Release #1.0, Version #1.30

APPLICATION DATA:

PLICATION NUMBER: US/09/953,052

LING DATE: 14-Sep-2001

ASSIFICATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: 09/052,919

LING DATE: <Unknown>

PLICATION NUMBER: US 08/844,419

LING DATE: 18-APR-1997

PLICATION NUMBER: US 08/846,017

LING DATE: 25-APR-1997

PLICATION NUMBER: US 08/851,843

LING DATE: 06-MAY-1997

PLICATION NUMBER: US 08/854,050

LING DATE: 09-MAY-1997

PLICATION NUMBER: US 08/911,312

LING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/912,951

LING DATE: 14-AUG-1997

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LING DATE: 19-NOV-1997

PLICATION NUMBER: US 08/974,584

LING DATE: 19-NOV-1997

PLICATION NUMBER: WO PCT/US97/17618

LING DATE: 01-OCT-1997

PLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
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TOPOLOGY: linear
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; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;           Lingner, Joachim
;           Nakamura, Toru
;           Chapman, Karen B.
;           Morin, Gregg B.
;           Harley, Calvin
;           Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
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; LENGTH: 4015 base pairs
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Query Match 98.2%; Score 3933; DB 14; Length 4015;
Best Local Similarity 99.1%; Pred. No. 0;
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QY CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3601
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QY GGGCCAGCTTTTCTCACCAGGAGCCCGCTTCCACTCCCGACATAGGAATAGT 3721
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QY CCCTGTACACAGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAAAT 3901
Db CCCTGTACACAGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAAAT 3932
QY GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTGAAAAA 3961
Db GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTGAAAAA

RESULT 6
US-10-208-243-1
; Sequence 1, Application US/10208243
; Publication No. US2003004394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Imm
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA

mo sapiens

S
6)..(3454)

ATION: human telomerase reverse transcriptase (hTERT)

ilarity 98.2%; Score 3933; DB 14; Length 4015;
Conservative 99.1%; Pred. No. 0;
Mismatches 0; Indels 36; Gaps 1;

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Db 901 CACCTCTTTGGAGGGTGGCTCTCTGGCACGGCCACTCCCAACCATCCGTGG

Qy 968 GCACACGCGGGCCCCCATCCACATCGCGGCCACCAACGTCCTCTGGACACGC

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Db 1441 CGGCTTCTGTGGGGCTGCTGCGCGGCTGCTGCGCCCCCAGGCTCTGGGGCTC

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AGATCCTCCTGCTGCAGCGGTACAGGTTTTCAGCATGTGTGCTGCAGTCCCATTTCA 3120

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Db 3121 TCAGCAAGTTTGGAAAGAACCCCAATTTTCTGCGGCTCATCTCTGACACGGC
QY 3152 CTGCTACTCCATCCTGAAAGCCAAAGAACGACGGGATGTCGCTGGGGGCCAAGG
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Db 3241 CGGCCCTCTGCCCTCCGAGGCCGTGACGTGGCTGTGCCACCAAGCATTCCTGCT
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RESULT 7
US-10-054-295-224
; Sequence 224, Application US/10054295
; Publication No. US2003004953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

OF INVENTION: No. US20030044953A1el Telomerase
OF SEQUENCES: 225
PONDENCE ADDRESS:
DRESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, 8th Floor
ITY: San Francisco
ATE: California
UNTRY: United States of America
P: 94111
R READABLE FORM:
DIUM TYPE: Floppy disk
MPUTER: IBM PC compatible
PERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: PatentIn Release #1.0, Version #1.30
T APPLICATION DATA:
PLICATION NUMBER: US/10/054,295
LING DATE: 18-Jan-2002
ASSIFICATION: 536
APPLICATION DATA:
PLICATION NUMBER: 08/854,050
LING DATE: <Unknown>
PLICATION NUMBER: US 08/846,017
LING DATE: 25-APR-1997
PLICATION NUMBER: US 08/844,419
LING DATE: 18-APR-1997
PLICATION NUMBER: US 08/724,643
LING DATE: 01-OCT-1996
Y/AGENT INFORMATION:
ME: Apple, Randolph T.
GISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
MUNICATION INFORMATION:
LEPHONE: (415) 576-0200
LEFAX: (415) 576-0300
FOR SEQ ID NO: 224:
NGTH: 4015 base pairs
PE: nucleic acid
RANDEDNESS: single
POLOGY: linear
E TYPE: cDNA
ME/KEY: CDS
CATION: 56..3454
HER INFORMATION: /product= "hTRT"
ote= "human telomerase reverse
anscriptase (hTRT) catalytic protein
mponent"
E DESCRIPTION: SEQ ID NO: 224:
4

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Conservative 99.1%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 36; Gaps 1;
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Db 241 ACGCGCGCCCCCGCGCCCCCTCTTCCGCGAGGTGTCTGCTGAAGGAGC
QY 308 CCGAGTGTGCGAGAGGTGTGCGAGCGCGCGCGGAAGAAAGTGTGCTGGCCTTCC
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us-09-424-686f-9.rnpb

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QY	2492	CAAGTCCTACGTCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCCACGC	
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RESULT 9
US-10-105-963-1
; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Com
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determina
; TITLE OF INVENTION: Recombination
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-105-963-1

Query Match 98.2%; Score 3933; DB 14; Length 4015;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36;
QY 8 GCAGCGTCCGTCCTGTCGCGACGTCGGGAGCCCTGGGAGCCCTGGGCGCCACCCCGC
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RESULT 10
US-10-044-692-1
; Sequence 1, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DJ
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
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UB-09-424-686f-9.rnpb

Similarity	98.2%;	Score 3933;	DB 14;	Length 4015;
Conservative	99.1%;	Pred. No. 0;		
		0; Mismatches	0; Indels	36; Gaps

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98.2%;	Score 3933;	DB 14;	Length 4015;
ilarity 99.1%;	Pred. No. 0;		
Conservative	0;	Mismatches	0; Indels 36; Gaps 1;
AGCGTGC	CGTCTCG	CACGTGG	GAAGCCCTGGCCCGGCACACCCCGCGATGCC 67
AGCGTGC	CGTCTCG	CACGTGG	GAAGCCCTGGCCCGGCACACCCCGCGATGCC 60
GCGTCC	CGCGCT	CGCGCT	CCCTGCTGCGCAGCCACTACCGGAGGTGCT 127
GCGTCC	CGCGCT	CGCGCT	CCCTGCTGCGCAGCCACTACCGGAGGTGCT 120
CGTGGC	CACGTT	CGTGG	CGCCCTGGGGCCCCCAGGGCTGGCGGCTGGTGCAGCGGG 187
CGTGGC	CACGTT	CGTGG	CGCCCTGGGGCCCCCAGGGCTGGCGGCTGGTGCAGCGGG 180

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Db	2401	GACCAGCCCGCTGAGGGATGCCGTCGTCTATCGAGCAGAGTCTCCTGAAATGA
QY	2432	CAGTGGCCTCTTCGACGCTCTTCTACGCTTTCATGTGCCACACGCGGTGCGCAT
Db	2461	CAGTGGCCTCTTCGACGCTCTTCTACGCTTTCATGTGCCACACGCGGTGCGCAT
QY	2492	CAAGTCCTACGTCAGTGCCAGGGATCCCGAGGGCTCCATCTCTCCACGCT
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QY	2552	CAGCCTGTGTACGGCGACATGGAGAACAAGCTGTTTGCGGGATTCGGCGGGA
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QY	2672	CTTCTCAGGACCTTGGTCCAGGTTGCCCTGAGTATGGTGCCTGGTGAACCTT
Db	2701	CTTCTCAGGACCTTGGTCCAGGTTGCCCTGAGTATGGTGCCTGGTGAACCTT
QY	2732	GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGT
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QY	2792	GCCGCCCCACGGCCTATTCCCTGGTGGCGCTGCTGCTGGATACCCGGACCCCT
Db	2821	GCCGCCCCACGGCCTATTCCCTGGTGGCGCTGCTGCTGGATACCCGGACCCCT
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Db	2941	CGGCTTCAAGGCTGGAGGAAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCT
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Db	3181	CTGCTACTCCATCCTGAAAGCCAAAGAACGACGGATGTGCTGGGGCCCAAGGG
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Db	3241	CGGCCCTCTGCCCTCCGAGGCCGTGAGTGGCTGTGCCACCAAGCATTCCTGCTC
QY	3272	GACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGACAGCCACG
Db	3301	GACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGACAGCCACG
QY	3332	GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGACGCAAC
Db	3361	GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGACGCAAC
QY	3392	ACTGCCCTCAGACTTCAAGACCATCTTGGAATGATGGCCACCCGCCACAGCCAG
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTTGGAATGATGGCCACCCGCCACAGCCAG

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RESULT 14

US-09-438-486-173
; Sequence 173, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
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; APPLICATION NUMBER: US 08/724,643
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; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:

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(415) 576-0300
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QY 3990 AAAAAAAAAAAAAA 4005
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3 Application US/10053758
US20030032075A1
INFORMATION:
INVENTOR: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
OF INVENTION: No. US20030032075A1el Telomerase
OF SEQUENCES: 225
OF SEQUENCE ADDRESS:
DRESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, 8th Floor
TY: San Francisco
ATE: California
UNTRY: United States of America
P: 94111
R READABLE FORM:
DIUM TYPE: Floppy disk
MPUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/10/053,758
LING DATE: 18-Jan-2002
ASSIFICATION: 536
PLICATION DATA:
PLICATION NUMBER: US/08/854,050
LING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/851,843
LING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/846,017
LING DATE: 25-APR-1997
PLICATION NUMBER: US 08/844,419
LING DATE: 18-APR-1997
PLICATION NUMBER: US 08/724,643
LING DATE: 01-OCT-1996
Y/AGENT INFORMATION:
ME: Apple, Randolph T.
GISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
MUNICATION INFORMATION:
LEPHONE: (415) 576-0200
LEFAX: (415) 576-0300
FOR SEQ ID NO: 173:
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NGTH: 4029 base pairs
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HER INFORMATION: /note= "preliminary sequence for
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CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTG 2045
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Db ||| 2334 CACGTCTCTACTTTCAGACACCTCCAGCCGTACATCGACAGTTCGTGGCTCAC
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QY ||| 2370 GAGACCAGCCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCCTCCCTGAAT
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Db ||| 2394 GANAACAGCCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCCTCCCTGAAT
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QY ||| 2430 AGCAGTGGCCTCTTCGACGCTCTTCTACGCTTCATGTGCCACACGCCGTGGC
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Db ||| 2454 AGCAGTGGCCTCTTCGACGCTCTTCTACGCTTCATGTGCCACACGCCGTGGC
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QY ||| 2490 GGCAAGTCTCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACC
|||
Db ||| 2514 GGCAAGTCTCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACC
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Db ||| 2574 TGCAGCCTGTCTACGGCGACATGGAGAACAAAGCTGTTTGGCGGGGATTCGGCGC
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Db ||| 2634 CTGCTCCTGCGTTTGGTGGATGATTTCTTGTGTGGTGCACCTCACCTCACCCAC
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QY ||| 2790 ATGCCGGCCACCGGCTATTCCCCTGTTGCGGCCCTGCTGCTGGATACCCGGACC
|||
Db ||| 2814 ATGCCGGCCACCGGCTATTCCCCTGTTGCGGCCCTGCTGCTGGATACCCGGACC
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Db ||| 3054 TACAAGATCCTCCTGCTGCAGGGGTACAGGTTTTCACGCTATGTGTGCTGAGCTC
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QY ||| 3210 GCCGGCCCTCTGCCCTCCGAGGCCGTGTCAGTGGCTGTGCCACCAAGCATTCCTG
|||
Db ||| 3234 GCCGGCCCTCTGCCCTCCGAGGCCGTGTCAGTGGCTGTGCCACCAAGCATTCCTG
|||
QY ||| 3270 CTGACTCGACACCGGTTCACCTACGTGCCACTCTCTGGGGTCACTCAGGACAGCC
|||

GACTGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGCG 3353
GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCGCGCAGCCAAACCCG 3389
GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCGCGCAGCCAAACCCG 3413
ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCC 3449
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GGCCAGCTTTTCTCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT 3749
GGCCAGCTTTTCTCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCAT 3773
CCAGATTGCCCATTTGTTACCCCTCGCCCTGCCCTCCTTGGCTTCCACCCCCACCAT 3809
CCAGATTGCCCATTTGTTACCCCTCGCCCTGCCCTCCTTGGCTTCCACCCCCACCAT 3833
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CCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGG 3929
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GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCACTTTTGAAAAAAA 3989
GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCACTTTTGAAAAAAA 4013

AAAAAAAAAAAA 4005
AAAAAAAAAAAA 4029

protein can be used in screening assays to identify of telomerase and to treat or inhibit cellular disorders, acts and/or other pathological processes involving telomerase, y cancer and ageing (also suitable for this are agents that inhibit or mimic the activity of the subunit). Antisense ds inhibit telomerase action (by binding to specific mRNA), y in neoplastic cells and may be expressed in vivo. Antibodies ts of the protein, used as probes or primers, are used to lomerase-related conditions (especially neoplasia) by (i) bnormal levels of the subunit protein in body fluids or (ii) by measuring the amount of the encoding nucleic acid. of the nucleic acid encoding the subunit mRNA is confined to s, in contrast to the ubiquitous expression of the telomerase

42 BP; 684 A; 1364 C; 1277 G; 717 T; 0 U; 0 Other;

98.9%; Score 3960; DB 2; Length 4042;

Conservative	0	Mismatches	0	Indels	36	Gaps	1
Conservative	0 <td>Mismatches</td> <td>0 <td>Indels</td> <td>36</td> <td>Gaps</td> <td>1</td> </td>	Mismatches	0 <td>Indels</td> <td>36</td> <td>Gaps</td> <td>1</td>	Indels	36	Gaps	1

'TTAGGCAGCGCTGCGTCCTGCTGCGCACGTGGAGCCCTGGCCCCGGCCACCCCG 60

"TTACGGCAGCGCTGCGTCTGTGGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCCG 60

!ATGCCGCGGCTCCCCGCTGCCGAGCCGTGGCTCCCTGCTGCGCAGCCACTACCGCG 12

ATGCCGCGCTCCCCGCTGCCGAGCCGTGCGTCCCTGCTGCGCAGCCACTACCGCG 120

GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGC 180

GTGCTGCCGCTGGCCACGTTCTGTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGC

CCGGGGA CCGGGGCTTTCCGGGGCTGGTGGCCAGTGGCTGGTGGCT 240

!CGCGGGAACCGGCGCTTTCGGCGCGTGGTGGCCAGTCCCTGGTGGCTGGCT 349

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913001

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1. *What is the main purpose of this study?*
 2. *What are the research objectives?*
 3. *What is the research methodology?*
 4. *What are the key findings?*
 5. *What are the limitations of the study?*
 6. *What are the implications of the study?*
 7. *What are the conclusions?*
 8. *What are the recommendations?*
 9. *What are the future research directions?*
 10. *What are the acknowledgments?*
 11. *What are the references?*
 12. *What are the appendices?*
 13. *What are the glossary?*
 14. *What are the abbreviations?*
 15. *What are the symbols?*
 16. *What are the units?*
 17. *What are the variables?*
 18. *What are the parameters?*
 19. *What are the constants?*
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ACGAGTGGCTCCAGCTGCCTCAGGTGTCGGCGCTGTTACCACTGGCG

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5'-GCCACTCAGGCCCGGCCACACGCTAGTGGACCCCGAAGCGTCTGGGATGCG 660

5'-GCCACTCAGGCCCGGCCCGCCACACGCTAGTGGACCCCGAAGCGTCTGGATCG-3'

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ACGGCCCTGGAACCATAGCGTCAGGAGGCCGGGTCCTCCCTGGGCTGCCAGCCCCGG 720

780 CAGAGGCGGGGGCAGTCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGGC

CGGAGGCGGGGCGAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGGC 780

QY	781	GTGGCGTGCCTTCTAGCCGGAGCGGACGCCGTTGGCAGGGTCTCTGGGCCC
DB	781	GTGGCGTGCCTTCTAGCCGGAGCGGACGCCGTTGGCAGGGTCTCTGGGCCC
QY	841	GCAGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACTGCGCAGA
DB	841	GCAGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACTGCGCAGA
QY	901	AAGAAGCCACCTCTTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCAACCCA
DB	901	AAGAAGCCACCTCTTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCAACCCA
QY	961	GCCGCCAGCACCAACGCGGGCCCCCATCCACATCGCGGCCACCAACGTCCTCTGG
DB	961	GCCGCCAGCACCAACGCGGGCCCCCATCCACATCGCGGGCCACCAACGTCCTCTGG
QY	1021	CTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTACTCTCAGGGGAC
DB	1021	CTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTACTCTCAGGGGAC
QY	1081	AGCTGGGCCCCCTCTTCTCTACTCAGCTCTCTGAGGCCCCAGCCCTGACTGSGCGCT
DB	1081	AGCTGGGCCCCCTCTTCTCTACTCAGCTCTCTGAGGCCCCAGCCCTGACTGSGCGCT
QY	1141	TCGTGAGACCATCTTTCTGGGTTCCAGGCCCTCGATGCCAGGGACTCCCCCGCT
DB	1141	TCGTGAGACCATCTTTCTGGGTTCCAGGCCCTCGATGCCAGGGACTCCCCCGCT
QY	1201	CCCGCTGCCCCCAGCGCTACTTGGCAATCGCGGCCCTGTTTCTGGAGCTGCTTT
DB	1201	CCCGCTGCCCCCAGCGCTACTTGGCAATCGCGGCCCTGTTTCTGGAGCTGCTTT
QY	1261	ACGCGAGTGCCCCCTACGCGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCT
DB	1261	ACGCGAGTGCCCCCTACGCGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCT
QY	1321	CCCCAGCAGCCGGTGTCTGTGCCCGGAGAGGCCCCAGGGCTCTGTGGCGGGCCC
DB	1321	CCCCAGCAGCCGGTGTCTGTGCCCGGAGAGGCCCCAGGGCTCTGTGGCGGGCCC
QY	1381	AGGAGGACACAGACCCCGCTGCGCTGGTGCACTGCTCCGCCAGCACAGCAGCAGC
DB	1381	AGGAGGACACAGACCCCGCTGCGCTGGTGCACTGCTCCGCCAGCACAGCAGCAGC
QY	1441	AGGTGTACGGCTTCGTGCGGGCCCTGCCCTGCGCGCGCTGGTGCCCCCAGGCCCT
DB	1441	AGGTGTACGGCTTCGTGCGGGCCCTGCCCTGCGCGCGCTGGTGCCCCCAGGCCCT
QY	1501	CCAGGCACAACGAACGCCCGCTTCTCTCAGGAACACCAAGAGTTTCATCTCCCTG
DB	1501	CCAGGCACAACGAACGCCCGCTTCTCTCAGGAACACCAAGAGTTTCATCTCCCTG
QY	1561	ATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCG
DB	1561	ATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCG
QY	1621	TGCGCAGGAGCCCAGGGTTGGCTGTGTTCCGGCCGCAGAGCAACCGTCTGCGCT
DB	1621	TGCGCAGGAGCCCAGGGTTGGCTGTGTTCCGGCCGCAGAGCAACCGTCTGCGCT
QY	1681	TCCTGGCCAAGTTCCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCF
DB	1681	TCCTGGCCAAGTTCCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCF
QY	1741	TCCTTTTATGTACGGAGACCACGTTTCAAAGAAACAGGCTCTTTTCTACCCGGA
DB	1741	TCCTTTTATGTACGGAGACCACGTTTCAAAGAAACAGGCTCTTTTCTACCCGGA
QY	1801	TCCTGGAGCAAGTTGCAAGACATTGGAATCAGACAGCACTTGAAGAGGGTGCAGC
DB	1801	TCCTGGAGCAAGTTGCAAGACATTGGAATCAGACAGCACTTGAAGAGGGTGCAGC
QY	1861	AGCTGTGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCTGCTGTF

andard; cDNA; 4037 BP.

(first entry)

erage reverse transcriptase encoding cDNA refined sequence.
merase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
eration; cancer; ageing; ribonucleoprotein; ss.

;

Location/Qualifiers
56..3454
/*tag= a
/product= "telomerase reverse transcriptase"
/note= "refined sequence"

; 97GB-00020890.

; 96US-00724643.
; 97US-00844419.
; 97US-00846017.
; 97US-00851843.
; 97US-00854050.
; 97US-00911312.
; 97US-00912951.
; 97US-00915503.

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V TECHNOLOGY CORP.

ingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

71633/16.
/56113.

combinant human Telomerase Reverse Transcriptase and its
are useful in the diagnosis, prognosis and treatment of cell
on conditions especially cancer and ageing.

Fig 74; 387pp; English.

sequence encodes human telomerase reverse transcriptase
ch is a ribonucleoprotein. The present invention also
he following methods: (A) determining whether a test compound
itor of hTERT, by detecting the change in hTERT recombinant
polynucleotide, on administration of the compound; (B)
of recombinant telomerase by contacting a protein preparation
h a telomerase RNA component; (C) detection of the hTERT RNA or
a sample by binding a relevant probe to the sample and
the complex formed or in the case of RNA detection, amplifying
and correlating the presence of complex or amplification
h presence of hTERT in the sample; and (D) increasing the
ion of a vertebrate cell by increasing hTERT expression; and (E)
an agent that causes an increase in cell vertebrate cell
ion to create a medicament that inhibits ageing. A protein
of hTERT and the polynucleotide encoding hTERT can be used in
ture of medicaments for inhibiting the effect of ageing or
ibitors of telomerase activity can be used to treat conditions
associated with high telomerase activity. A protein preparation
also be used in the new methods

SQ	Sequence	4037 BP; 682 A; 1362 C; 1275 G; 714 T; 0 U; 4 Other;
	Query Match	98.5%; Score 3945; DB 2; Length 4037;
	Best Local Similarity	98.9%; Pred. No. 0;
	Matches 3991; Conservative	4; Mismatches 4; Indels 36;
QY	8	GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCGC
Db	1	GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCGC
QY	68	GCGCGCTCCCCGCTGCCGAGCCGCTGCGTCCCTGCTGCGCAGCCACTACCGCGA
Db	61	GCGCGCTCCCCGCTGCCGAGCCGCTGCGTCCCTGCTGCGCAGCCACTACCGCGA
QY	128	GCCGCTGGCCACGTTCTGTCGGCGCCTGGGGCCCCCAGGGCTGGCGGCTGGTGCA
Db	121	GCCGCTGGCCACGTTCTGTCGGCGCCTGGGGCCCCCAGGGCTGGCGGCTGGTGCA
QY	188	GGACCCGCGGCTTTCCGCGCGCTGGTGGCCCCAGTGCCTGGTGTGCGTGCCCTG
Db	181	GGACCCGCGGCTTTCCGCGCGCTGGTGGCCCCAGTGCCTGGTGTGCGTGCCCTG
QY	248	ACGCGCGCCCCCGCCGCCCTCTCTCCGCCAGGTGCTGCTGCTGAAGGAGCT
Db	241	ACGCGCGCCCCCGCCGCCCTCTCTCCGCCAGGTGCTGCTGCTGAAGGAGCT
QY	308	CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGAAGAACGTCCTGGCCTTCGG
Db	301	CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGAAGAACGTCCTGGCCTTCGG
QY	368	GCTGCTGGACGGGGCCCCGGGGGCCCCCGAGGCCCTTCACCCAGCGTGC
Db	361	GCTGCTGGACGGGGCCCCGGGGGCCCCCGAGGCCCTTCACCCAGCGTGC
QY	428	CTGCCCCAACACGCTGACCGACGCTGCGGGGGAGCGGGGCGTGGGGGCTGC
Db	421	CTGCCCCAACACGCTGACCGACGCTGCGGGGGAGCGGGGCGTGGGGGCTGC
QY	488	CCGCGTGGGCGACGACGTCGTGCTGCTTACCTGTGGCACGCTGCGCGCTCTTTG
Db	481	CCGCGTGGGCGACGACGTCGTGCTTACCTGTGGCACGCTGCGCGCTCTTTG
QY	548	GGCTCCCGAGCTGCGCTTACAGGTGTGCGGGCCGCGCTGTGTACAGCTCGGCG
Db	541	GGCTCCCGAGCTGCGCTTACAGGTGTGCGGGCCGCGCTGTGTACAGCTCGGCG
QY	608	TCAGGCCCCGGCCCCCGCACAGCTAGTGGACCCCGGAGGCGTCTGGGATGCG
Db	601	TCAGGCCCCGGCCCCCGCACAGCTAGTGGACCCCGGAGGCGTCTGGGATGCG
QY	668	CTGGAACCATAGCGTCAAGGAGCGCGGGTCCCGCTGCGCGCTGCGACCCCGG
Db	661	CTGGAACCATAGCGTCAAGGAGCGCGGGTCCCGCTGCGCGCTGCGACCCCGG
QY	728	GAGCGCGGGGGCAGTGCCAGCCGAAAGTCTGCCGTTGCCCAAGAGGCCCCAGGC
Db	721	GAGCGCGGGGGCAGTGCCAGCCGAAAGTCTGCCGTTGCCCAAGAGGCCCCAGGC
QY	788	TGCCCTGAGCCGAGCGGAGCGCGCTTGGGAGGGGTCTTGGGGCCCCACCCGG
Db	781	TGCCCTGAGCCGAGCGGAGCGCGCTTGGGAGGGGTCTTGGGGCCCCACCCGG
QY	848	GCGTGGACCGAGTGACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db	841	GCGTGGACCGAGTGACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
QY	908	CACCTCTTTGGAGGGTGGCTCTTGGCACGCGCCACTCCACCCCATCCGTGG
Db	901	CACCTCTTTGGAGGGTGGCTCTTGGCACGCGCCACTCCACCCCATCCGTGG
QY	968	GCACACGCGGGCCCCCATCATCATCGCGGCCACCCAGTCCCTGGGACACGC
Db	961	GCACACGCGGGCCCCCATCATCATCGCGGCCACCCAGTCCCTGGGACACGC

|||||GCTACTCATCTCTGAAAGCCAAAGAACGACGAGGATGTCGCTGGGGCCAAAGGGCGCGC 3240
|||||GCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271
|||||GCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
|||||CTCGACACCGTGTACCTACGTGACCACTCCTGGGGTCACTCAGACAGCCAGACGCA 3331
|||||CTCGACACCGTGTACCTACGTGACCACTCCTGGGGTCACTCAGACAGCCAGACGCA 3360
|||||TGAGTCGGAAGCTCCCGGGACGACGCTGACCTGCCCTGGAGCGCGCAGCCAAACCCGGC 3391
|||||TGAGTCGGAAGCTCCCGGGACGACGCTGACCTGCCCTGGAGCGCGCAGCCAAACCCGGC 3420
|||||TGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCGCCACAGCCAGGCGCA 3451
|||||TGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCGCCACAGCCAGGCGCA 3480
|||||GCAGACACGACGACGCTGTACGCGCGGCTCTACGTCCCGAGGAGGGCGCGCC 3511
|||||GCAGACACGACGACGCTGTACGCGCGGCTCTACGTCCCGAGGAGGGCGCGCC 3540
|||||CACCCAGGCGCGCACGCTGGAGTCTGAGGCTGAGTGAGTGTGGCCGAGGCGCTG 3571
|||||CACCCAGGCGCGCACGCTGGAGTCTGAGGCTGAGTGAGTGTGGCCGAGGCGCTG 3600
|||||TGTCGCGGTGAAGGCTGAGTGTCCCGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3631
|||||TGTCGCGGTGAAGGCTGAGTGTCCCGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3660
|||||GTGTCAGACACCTGCCGTCTTCACTTCCCCACAGGCTGGCTGGCTCCACCCCA 3691
|||||GTGTCAGACACCTGCCGTCTTCACTTCCCCACAGGCTGGCTGGCTCCACCCCA 3720
|||||GCCAGCTTTCTCACCAGGAGCCCGGCTTCCACTCCCGACATAGGAATAGTCCATCC 3751
|||||GCCAGCTTTCTCACCAGGAGCCCGGCTTCCACTCCCGACATAGGAATAGTCCATCC 3780
|||||AGATTGCGCATTTGTTCAACCCCTCGCCCTGCGCTTCCCTTCCACCCCGCCATCC 3811
|||||AGATTGCGCATTTGTTCAACCCCTCGCCCTGCGCTTCCCTTCCACCCCGCCATCC 3840
|||||GTGGAGACCTTGAGAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3871
|||||GTGGAGACCTTGAGAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3900
|||||CTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3931
|||||CTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960
|||||GGTGTGTGGAGTAAATACTGAATATATAGTTTTTCAGTTTGAATAAAAAA 3991
|||||GGTGTGTGGAGTAAATACTGAATATATAGTTTTTCAGTTTGAATAAAAAA 4020
|||||AAAAAAAAAAAA 4006
|||||AAAAAAAAAAAA 4035

standard; cDNA; 4023 BP.

3 (first entry)

nerase gene referred to as hEST2.

subunit; human; telomerase; telomere maintenance; diagnosis;
cancer; ss.

OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 59..3458
FT /*tag= a
FT
XX WO9837181-A2.
PN
XX 27-AUG-1998.
PD
XX 20-FEB-1998; 98WO-US003404.
PF
XX 20-FEB-1997; 97US-0038750P.
PR 20-MAY-1997; 97US-0047151P.
PR 01-AUG-1997; 97US-0054549P.
PR 14-AUG-1997; 97US-0055762P.
PR 30-OCT-1997; 97US-0064322P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Counter CM, Meyerson M, Weinberg RA;
PI
XX WPI; 1998-495367/42.
DR P-PSDB; AAW71376.
DR
XX
PT New isolated human telomerase catalytic sub-unit gene - used to
PT products for increasing or reducing the life span of cells such
PT cells or transformed cells.
XX
PS Claim 5; Fig 5A-B; 96pp; English.
XX
CC The present sequence encodes the catalytic subunit of a human t
CC holoenzyme. Disruption of the telomerase gene alters telomere
CC maintenance. The DNA is essential for telomerase activity, and
CC protein is physically associated with telomerase and a constit
CC active telomerase complex. The products can be used for increa
CC reducing the lifespan of cells such as cancer cells or transfo
CC They can also be used in the diagnosis and treatment of malign
CC addition, cells with a longer lifespan can be transplanted into
CC grafted onto an individual (e.g. as skin grafts, as systems for
CC of therapeutic proteins, such as hormones and enzymes), to whom
CC provide therapeutic benefit
XX
SQ Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 U; 0 Other;
Query Match 98.3%; Score 3937.8; DB 2; Length 4023;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3985; Conservative 0; Mismatches 2; Indels 36;
QY 5 CAGGACGCGTGGCTCTCTGCTGCGACGCTGGGAAGCCCTGGCCCGCCACCC
Db
QY 1 CAGGACGCGTGGCTCTCTGCTGCGACGCTGGGAAGCCCTGGCCCGCCACCC
Db
QY 65 GCCGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTGCGGAGCCACTACC
Db
QY 61 GCCGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTGCGGAGCCACTACC
QY 125 GCTGCGCTGGCCACGTTCTGCGGCGCTGGGGCCCGAGGCTGGCGGTGG
Db
QY 121 GCTGCGCTGGCCACGTTCTGCGGCGCTGGGGCCCGAGGCTGGCGGTGG
QY 185 CGGGACCGCGCGGCTTTCGCGCGCTGGTGGCCAGTGCCTGCTGCTGCTGC
Db
QY 181 CGGGACCGCGCGGCTTTCGCGCGCTGGTGGCCAGTGCCTGCTGCTGCTGC
QY 245 CGCACGCGCGCGCGCGCGCGCGCGCTTTCGCGCGAGTGTCTGCTGAAGG
Db
QY 241 CGCACGCGCGCGCGCGCGCGCGCGCTTTCGCGCGAGTGTCTGCTGAAGG
QY 305 GGCCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGGAGAACGCTGCTGGCCT
Db
QY 301 GGCCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGGAGAACGCTGCTGGCCT

09:53:30 2004

us-09-424-686f-9.rng

CGCTGTGGACGGGGCCCGCGGGGGCCCCCCCCGAGGCCTTCAACCAACGAGCGTGGCGCAG	424
CGCTGTGGACGGGGCCCGCGGGGGCCCCCCCCGAGGCCTTCAACCAACGAGCGTGGCGCAG	420
ACCTGCCCAACACCGGTACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGTGCTGCT	484
ACCTGCCCAACACCGGTACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGTGCTGT	480
3CGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCACGCTGCGCGCTCTTTGTGCT	544
3CGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCACGCTGCGCGCTCTTTGTGCT	540
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TGGTCCAGCTGCGCCTACCAAGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCTGC	600
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CTCAGGCCCGGCCCCCCACACGCTAGTGGAACCCGAAGCGCTCTGGGATGCGAACG	660
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CTTGGAACCATAGCGTCAGGAGGCCGGGTCCCCCTGGGCTGCCAGCCCCGGGTGC	720
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CTGCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCTGGGCCCAACCCGGGCGAG	840
CGCGTGGACCGAGTGACCGTGTTCTGTGTGTGTCACTGCCAGACCCGCCCGGAAGA	904
CGCGTGGACCGAGTGACCGTGTTCTGTGTGTGTCACTGCCAGACCCGCCCGGAAGA	900
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CCACTCTTTGGAGGTGCGTCTCTTGGCACGGCCACTCCCAACCCATCCGTGGGCGG	960
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CCCCGCTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGCGGACCAAGGAGCAGCT	1080
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ACGGCTTGTGCGGGCCTGCCCTGCGCGGGCTGGTGCCCGCAGGCCCTCTGGGGCTCCAG	1504

Db	1441		GTACGGCTTCGTGCGGCCTGCCCTGCGCCGGCTGGTGCCCCCAGGCCCTCTGGG
Qy	1505		GCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGAA
Db	1501		GCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGAA
Qy	1565		CAAGCTCTCGCTGACGAGGCTGACGTTGGAAGATGAGCGTGCGGGAAGTGCCTTC
Db	1561		CAAGCTCTCGCTGACGAGGCTGACGTTGGAAGATGAGCGTGCGGGAAGTGCCTTC
Qy	1625		CAGGAGCCCAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGGA
Db	1621		CAGGAGCCCAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGGA
Qy	1685		GGCCAAAGTTCTTGCACTGGCTGATGAGTGTGTACGTCTGTCGAGCTGCTCAGGTC
Db	1681		GGCCAAAGTTCTTGCACTGGCTGATGAGTGTGTGTACGTCTGTCGAGCTGCTCAGGTC
Qy	1745		TTATGTACGGAGACCAAGCTTTCAAAGAACAAGGCTCTTTTCTACCGGAAGAG
Db	1741		TTATGTACGGAGACCAAGCTTTCAAAGAACAAGGCTCTTTTCTACCGGAAGAG
Qy	1805		GAGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCC
Db	1801		GAGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCC
Qy	1865		GTCGGAAGCAGAGTTCAGGCAGCATCCGGGAAGCCAGGCCCGCCCTGCTGACGTC
Db	1861		GTCGGAAGCAGAGTTCAGGCAGCATCCGGGAAGCCAGGCCCGCCCTGCTGACGTC
Qy	1925		CCGCTTCATCCCCAAGCTTGACGGCTGCGGCCGATTTGTGAACATGGACTACGTA
Db	1921		CCGCTTCATCCCCAAGCTTGACGGCTGCGGCCGATTTGTGAACATGGACTACGTA
Qy	1985		AGCCAGAACGTTCCGCAGAGAAAGAGGSCGAGCGCTCTCACCTCGAGGGTGA
Db	1981		AGCCAGAACGTTCCGCAGAGAAAGAGGSCGAGCGCTCTCACCTCGAGGGTGA
Qy	2045		GTTCAGCGTGCTCAACTACGAGCGGGCGGCGCCCCCGCCCTCCTGGGCGCCTC
Db	2041		GTTCAGCGTGCTCAACTACGAGCGGGCGGCGCCCCCGCCCTCCTGGGCGCCTC
Qy	2105		GGGCTTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGC
Db	2101		GGGCTTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGC
Qy	2165		CCGCGCCCTGAGCTGTA-----
Db	2161		CCGCGCCCTGAGCTGTA-----
Qy	2189		CCAGGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAAACACGTA
Db	2221		CCAGGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAAACACGTA
Qy	2249		GGCTCGGTATGCCGTGGTCCAGAGGCGCGCCATGGGCACGTCCGCAAGGCCTTA
Db	2281		GGCTCGGTATGCCGTGGTCCAGAGGCGCGCCATGGGCACGTCCGCAAGGCCTTA
Qy	2309		CCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGGCACAGTTCTGTTGGCTCA
Db	2341		CCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGGCACAGTTCTGTTGGCTCA
Qy	2369		GGAGACACAGCCCGTGGGGATGCCGTCTGTCATCGAGCAGAGTCTCCTCCCTGAA
Db	2401		GGAGACACAGCCCGTGGGGATGCCGTCTGTCATCGAGCAGAGTCTCCTCCCTGAA
Qy	2429		CAGCAGTGGCCTCTTCACAGCTCTTCTTACGCTTCATGTGCCACACACCGCTGCC
Db	2461		CAGCAGTGGCCTCTTCACAGCTCTTCTTACGCTTCATGTGCCACACACCGCTGCC
Qy	2489		GGSCAAGTCTTACGTCCAGTGCCAGGGGATCCCGAGGGCTCCATCTCTCTCCAC

GCAAGTCCTACGTCCAGTGCAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCT 2580
GCAGCTGTGCTACGGCGACATGGAGAAACAAGCTGTTTGGGGGATTCCGGGGACGG 2608
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TGCTCTGCTGTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGGGAA 2668
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TGACAGCGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAA 2908
TGACAGCGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAA 2940
GCGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGGGCTGAA 2968
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GCATGTCGGCTGAAGGCTGAGTTCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3628
GCATGTCGGCTGAAGGCTGAGTTCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660

QY 3629 GCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGC
Db 3661 GCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGC
QY 3689 CCAGGGCCAGCTTTTCTCAACAGGAGCCCGGCTTCCACTCCCCACATAGGAAT
Db 3721 CCAGGGCCAGCTTTTCTCAACAGGAGCCCGGCTTCCACTCCCCACATAGGAAT
QY 3749 TCCCCAGATTGCGCAATGTTTCAACCCCTGCCCTGCCCTTCCCTTTGCCCTTCCACCC
Db 3781 TCCCCAGATTGCGCAATGTTTCAACCCCTGCCCTGCCCTTCCCTTTGCCCTTCCACCC
QY 3809 TCCAGGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACC
Db 3841 TCCAGGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACC
QY 3869 GTGCCCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCA
Db 3901 GTGCCCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCA
QY 3929 GGGGAGGTGCTGTGGAGTAAATACTGAATATATAGTTTTTCAGTTTGA
Db 3961 GGGGAGGTGCTGTGGAGTAAATACTGAATATATAGTTTTTCAGTTTGA
QY 3989 AAA 3991
Db 4021 AAA 4023

RESULT 4
ABL53711

ID ABL53711 standard; cDNA; 4070 BP.

XX ABL53711;

AC ABL53711;

XX 17-JUN-2002 (first entry)

DT 17-JUN-2002 (first entry)

XX Human telomerase catalytic subunit hTERT cDNA.

DE hTERT; telomerase; reverse transcriptase; immortalisation; huma

XX hTERT; telomerase; reverse transcriptase; immortalisation; huma

KW vaccine; enzyme; gene; ss.

XX Homo sapiens.

OS WO200216555-A2.

XX 28-FEB-2002.

PN 17-AUG-2001; 2001WO-GB003726.

XX 17-AUG-2000; 2000GB-00020246.

PD 17-AUG-2000; 2000US-0225734P.

XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.

PA Jones CJ, Kipling DG, Wilkinson G, Mosharry B, Skinner JW;

XX WPI; 2002-315462/35.

DR Novel hTERT-immortalized cell line (human telomerase reverse

XX transcriptase) useful for human vaccine production and preparat

PT antigen, such as a virus or virus-derived agent.

XX Example 1; Fig 1; 64pp; English.

PS The present sequence is that of hTERT cDNA in plasmid pGRN121.

XX the catalytic subunit of human telomerase. Claimed immortalised

CC lines for use in vaccine production are adapted to express hTER

CC Suitable cell lines comprise human diploid fibroblasts, e.g. MR

CC WI38 cells, transfected with hTERT cDNA or infected by a retrov

CC carrying hTERT cDNA, and are capable of supporting antigen prod

CC method for preparing such cell lines using recombinant techniqu

The cell lines are also used as a diagnostic test for the
f a virus, such as human cytomegalovirus, and to determine the
antiviral agents by testing the capability of a modified
aining a reporter gene to infect the cells. The cell lines have
y, which can be impaired in cell lines immortalised by other
f, being able to support viral replication. The cells remain
cally suitable for viral/vaccine cultivation

370 BP; 670 A; 1383 C; 1296 G; 721 T; 0 U; 0 Other;

98.2%; Score 3933.4; DB 6; Length 4070;

ilarity 99.1%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 36; Gaps 1;

3GCAGCGTCCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGCCACCCCGGATG 65

3GCAGCGTCCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCCGCCACCCCGGATG 78

3GCGCGTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGGCGAGCCACTACCGGAGGTG 125

3GCGCGTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGGCGAGCCACTACCGGAGGTG 138

TGCCGCTGGCCACGTTCTGTCGGCGCTGGTGGGCCCCAGGGCTGGCGGTGGTGCAGCGC 185

TGCCGCTGGCCACGTTCTGTCGGCGCTGGTGGGCCCCAGGGCTGGCGGTGGTGCAGCGC 198

3GGACCCGGCGGCTTTCCGCGCGCTGGTGGGCCCCAGTGGCTGGTGCCTGGGAC 245

3GGACCCGGCGGCTTTCCGCGCGCTGGTGGGCCCCAGTGGCTGGTGCCTGGGAC 258

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CACGGCCGCCCGCCCGCTCCCTTCCGCCAGGTCTCTGCCTGAAGGAGTGGTG 318

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CCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGGAGAACGTGCTGGCTTC 378

3GCTGTGGACGGGGCCCGGGGGCCCCCGAGGCTTACCAACAGCTGGCGCAGC 425

3GCTGTGGACGGGGCCCGGGGGCCCCCGAGGCTTACCAACAGCTGGCGCAGC 438

ACCTGCCCAACACGGTGACCGACGCACCTGCGGGGAGCGGGCTGGCTGTG 485

ACCTGCCCAACACGGTGACCGACGCACCTGCGGGGAGCGGGCTGGCTGTG 498

3CCGCGTGGCGACGAGTGTGGTTACCTGTGGCACGCTGCGCGCTCTTGTGCTG 545

3CCGCGTGGCGACGAGTGTGGTTACCTGTGGCACGCTGCGCGCTCTTGTGCTG 558

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TGGCTCCAGCTGCGCTACAGGTGTGCGGGCCCGCGCTGTACAGCTGGCGCTGCC 618

3TCAGGCCCGCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGG 665

3TCAGGCCCGCCCGCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGG 678

3CTGGAACCATAGCGTCAGGGAGGCCGGGTCCCGCTGGGCTGCCAGCCCGGGTGGC 725

3CTGGAACCATAGCGTCAGGGAGGCCGGGTCCCGCTGGGCTGCCAGCCCGGGTGGC 738

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3GAGGCGGGGGCAGTGCCAGCCGAAAGTCTGCCGTGGCCCAAGAGGCCAGGCGTGGC 798

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3TGCCCTGAGCCGAGCGGACGCCCGTTGGCGAGGGTCTTGGGCCACCCGGGACGG 858

3GCGTGGACCGAGTACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCGCCGAAGAA 905

3GCGTGGACCGAGTACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCGCCGAAGAA 918

QY 906 GCCACCTCTTTGGAGGTGGCTCTCTGGCACGCGCCACTCCCAACCCATCCGT

Db 919 GCCACCTCTTTGGAGGTGGCTCTCTGGCACGCGCCACTCCCAACCCATCCGT

QY 966 CAGCACACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACAC

Db 979 CAGCACACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACAC

QY 1026 CCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGGA

Db 1039 CCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGGA

QY 1086 CGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGGCGCTCGGAC

Db 1099 CGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGGCGCTCGGAC

QY 1146 GAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCGAGGT

Db 1159 GAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCGAGGT

QY 1206 CTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAA

Db 1219 CTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAA

QY 1266 CAGTGCCCCCTACGGGGTGTCTCTCAAGACGACTGCCCCGCTGCGAGCTGCGGT

Db 1279 CAGTGCCCCCTACGGGGTGTCTCTCAAGACGACTGCCCCGCTGCGAGCTGCGGT

QY 1326 GCAGCCGGTGTCTGTGCCCCGGGAGAACCCAGGGCTCTGTGGCGGCCCCGA

Db 1339 GCAGCCGGTGTCTGTGCCCCGGGAGAACCCAGGGCTCTGTGGCGGCCCCGA

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Db 1399 GACACAGACCCCGCTGCTGGTGAGCTGCTCGCCAGCACAGCAGCCCTG

QY 1446 TAGGGCTTCGTGCGGGCTGCTGCTGCGCGGCTGCTGCCCCAGGCCCTCTGGG

Db 1459 TAGGGCTTCGTGCGGGCTGCTGCTGCGCGGCTGCTGCCCCAGGCCCTCTGGG

QY 1506 CACAACGAACGCGCTTCTCAGGAACACCAAGAAGTTTCTCTCCCTGGGAA

Db 1519 CACAACGAACGCGCTTCTCAGGAACACCAAGAAGTTTCTCTCCCTGGGAA

QY 1566 AAGCTCTCGTGCAGGAGCTGACGTGGAAAGATGAGCGTGGGACTGCGCTTG

Db 1579 AAGCTCTCGTGCAGGAGCTGACGTGGAAAGATGAGCGTGGGACTGCGCTTG

QY 1626 AGGAGCCCGGGTGGTGTTCGGCCGCGAGAGCACCGTCTGCGTGAGGA

Db 1639 AGGAGCCCGGGTGGTGTTCGGCCGCGAGAGCACCGTCTGCGTGAGGA

QY 1686 GCCAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCGTTCGAGCTGCTCAGTC

Db 1699 GCCAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCGTTCGAGCTGCTCAGTC

QY 1746 TATGTACGGGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGGAGAG

Db 1759 TATGTACGGGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGGAGAG

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QY 1866 TCGGAAGCAGAGGTGAGGAGCATTCGGGAAGCCAGGCCCGCTGCTGACGTC

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QY 1926 CGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGT

Db 1939 CGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGT

catalytic domain; human; quantitation; tumour cell; melanoma;
metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
atic leukemia; melanoma; pulmonary carcinoma; colon cancer;
er; ss.

1s.
-A1.
3.
3; 98DE-01004372.
3; 98DE-01004372.
JM M W.

131408/37.

tumor cells by amplifying mRNA encoding the catalytic subunit
ase.

-g 1A-B; 26pp; German.

ion describes a novel method for the quantitation of tumour
body fluid which comprises (1) enrichment or isolation of
s in the sample, (2) amplification of mRNA from these cells
s the catalytic subunit of telomerase and (3) quantifying the
mplified mRNA. The method is applied to tumour cells derived
)metastases, e.g. associated with a wide range of tumours such
-lymphoblastoma, chronic myeloid or acute lymphatic leukemia,
pulmonary carcinoma, cancer of colon or breast etc. This
icodes a human telomerase protein catalytic domain

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

98.2%; Score 3933; DB 2; Length 4015;

ilarity 99.1%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 36; Gaps 1;

AGCGTGGCTGCTGCGACGCTGGGAGCCCTGGCCCCGCCACCCCGCATGCC 67

AGCGTGGCTGCTGCGACGCTGGGAGCCCTGGCCCCGCCACCCCGCATGCC 60

GGCTCCCCGCTGCGAGCCGCTCCCTGCTGCGAGCCACTACCGGAGGTGCT 127

GGCTCCCCGCTGCGAGCCGCTCCCTGCTGCGAGCCACTACCGGAGGTGCT 120

GGCTGGCCACGTTGCTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCG 187

GGCTGGCCACGTTGCTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCG 180

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DE Human hTERT gene.
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376930/40.

ag expression of mRNA encoding hTERT, the catalytic subunit of
, as an indicator of cancer, by amplifying RNA using primers
ary to hTERT gene sequence and quantitating amplified products.

age 5-7; 29pp; English.

sequence is that of the hTERT gene encoding the catalytic
the human telomerase, comprising 16 exons, which is useful in
or quantitating hTERT mRNA. The method is useful for detecting
ce of beta-region (a 182 nucleotide region consisting of exons
f the hTERT-mRNA in a human sample for diagnosis and prognosis
The method provides an accurate measure of telomerase activity
vely measuring mRNA that encodes an active hTERT protein

015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

98.2%; Score 3933; DB 4; Length 4015;

ilarity 99.1%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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standard; cDNA; 4015 BP.

. (first entry)

erase reverse transcriptase (TERT) cDNA.

α antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
α alpha(1,2)fucosyltransferase; alpha1,2FT; human;
reverse transcriptase; gene: ss.

15.

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-A2.

[illegible]

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QY 3932 GAGGTGCTGTGGGAGTAAATACTGAATATATAGTATTTTTCAGTTTGAATA/

Db 3961 GAGGTGCTGTGGGAGTAAATACTGAATATATAGTATTTTTCAGTTTGAATA/

RESULT 10

ABA97534

ID ABA97534 standard; DNA; 4015 BP.

XX ABA97534;

AC ABA97534;

DT 05-APR-2002 (first entry)

XX Cancer cell discrimination method related human DNA.

DE Human; telomerase; enzyme; cancer cell discrimination; gene;

XX reverse transcriptase; ds.

KW Homo sapiens.

OS JP2001309791-A.

PN 06-NOV-2001.

XX 02-MAY-2000; 2000JP-00138250.

PF 02-MAY-2000; 2000JP-00138250.

PR (KANE/) KANEUCHI H.

XX (KAMI/) KAMIMORI M.

DR WPI; 2002-134853/18.

XX Discrimination of a cancer cell in a sample tissue, comprises the expression level of a reverse transcriptase component of t using a hybridization assay.

PS Claim 2; Page 9-10; 16pp; Japanese.

XX The present invention relates to a method for the discrimination of a cancer cell in a sample tissue, which involves determining the level of a reverse transcriptase component of telomerase in a constituting the sample tissue by an in situ hybridization of the enzyme, and judging a cell showing a higher expression level that of the reverse transcriptase component of telomerase in a cell to be a cancer cell. The present sequence is a human DNA exemplification of the invention

SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 98.2%; Score 3933; DB 6; Length 4015;

Best Local Similarity 99.1%; Pred. No. 0;

Matches 3979; Conservative 0; Mismatches 0; Indels 36;

QY 8 GCAGCGTCCCGCTGCTGTCGCGACGCTGGGAGCCCTGGCCCCGCCACCCCGC

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QY 68 GCGCGTCCCGCTGCTGTCGCGACGCTGGGAGCCCTGGCCCCGCCACCCCGC

Db 61 GCGCGTCCCGCTGCTGTCGCGACGCTGGGAGCCCTGGCCCCGCCACCCCGC

QY 128 GCGCGTGGCCACGTTCTGTCGCGCGCTGGGAGCCCTGGCCCCGCCACCCCGC

Db 121 GCGCGTGGCCACGTTCTGTCGCGCGCTGGGAGCCCTGGCCCCGCCACCCCGC

QY 188 GGACCCGCGGCTTTCCGCGCGCTGGTGGGCCAGTGGCTGGTGGCTGGCTGGCTG

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US-09-424-686f-9.rnq

[illegible]

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Db	1381	CACAGACCCCGTCGCGCTGGTGCACTGCTCCGCCAGCACACAGCAGCCCTTGCG
QY	1448	CGGCTTCGTGCGGGCTGCCTGCGCCGGCTGGTGCCCCCAGGCCCTCTGGGGCT
Db	1441	CGGCTTCGTGCGGGCTGCCTGCGCCGGCTGGTGCCCCCAGGCCCTCTGGGGCT
QY	1508	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAAGTTTCACTCTCCTTGGGGAAGC
Db	1501	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAAGTTTCACTCTCCTTGGGGAAGC
QY	1568	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGCGGGAACCTGCGCTTGCG
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Db	2161	GCCGCCCTGAGCTGTA-----CAM
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Db	2221	GGACAGGCTCAGGAGTTCATCGCCAGCATCATCAAAACCCAGAACACGCTACTG
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Db	2281	TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCCTTCA
QY	2312	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTTCGTGGCTCACCT
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QY 3632 GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCAACAGGCTGGCGCTCGGCTC
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Db 3661 GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCAACAGGCTGGCGCTCGGCTC
|||||
QY 3692 GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAG
|||||
Db 3721 GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAG
|||||
QY 3752 CCAGATTCCGCATTGTTCAACCCCTCGCCCTGCCCCTCCTTTGCCCTTCCACCCCC
|||||
Db 3781 CCAGATTCCGCATTGTTCAACCCCTCGCCCTGCCCCTCCTTTGCCCTTCCACCCCC
|||||
QY 3812 AGGTGGAGACCTTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAA
|||||
Db 3841 AGGTGGAGACCTTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAA
|||||
QY 3872 CCCTGTACACAGCGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAA
|||||
Db 3901 CCCTGTACACAGCGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAA
|||||
QY 3932 GAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTTCAGTTTGAAGAAA
|||||
Db 3961 GAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTTCAGTTTGAAGAAA
|||||
RESULT 11
ACCS58039
ID ACC58039 standard; cdna; 4015 BP.
XX
AC ACC58039;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase cdna.
XX
KW Telomerase reverse transcriptase; TERT; enzyme; RNA interferen
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; conti
KW immunosuppressive; antiinfertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 56..3454
FT /*tag= a
FT /product= "TERT"
XX
PN WO2003035667-A2.
XX
PD 01-MAY-2003.
XX
PF 16-OCT-2002; 2002WO-US033065.
XX
PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Rowley PT;
XX

03336/38.
42384.

le-stranded short interfering RNA having sense and antisense
ids which are complementary to each other and to target nucleic
telomerase RNA or mRNA encoding telomerase reverse
ise.

: Fig 3A-B; 37pp; English.

: sequence is that of human telomerase reverse transcriptase
a. The invention relates to the discovery that double-stranded
RNAs, such as short interfering RNAs (siRNA), which target
RNA or TERT mRNA are capable of inhibiting telomerase
inhibition of telomerase in cancer cells leads to telomere
end-to-end chromosomal fusion, and apoptosis. Interference of
activity can also be used for treatment of infertility, for
on or sterilisation, for immunosuppression, for treatment of
site and fungal infections, and in antiinflammatory therapies.
ise is active in a limited number of cell types, e.g. tumour
line cells, certain stem cells of the haematopoietic system, T
s, sun-damaged skin, and proliferative cervix, most normal
ot affected by telomerase RNA interference therapy

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

ilarity 98.2%; Score 3933; DB 7; Length 4015;

Conservative 0; Mismatches 0; Indels 36; Gaps 1;

AGCGTGGCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCCCGCATGCC 67
AGCGTGGCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCCACCCCGCATGCC 60
GCGTCCCCCGTGGCGAGCCGTGCGTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 127
GCGTCCCCCGTGGCGAGCCGTGCGTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 120
CGCTGGCCACGTTCTGCGGCGCCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGCG 187
CGCTGGCCACGTTCTGCGGCGCCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGCG 180
ACCGGGCGGCTTCCGCGCGCTGGTGGCCCGCAGTGCCTGGTGGCGTGCCTGGGACGC 247
ACCGGGCGGCTTCCGCGCGCTGGTGGCCCGCAGTGCCTGGTGGCGTGCCTGGGACGC 240
GGCCGCCCGCCCGCCCGCCCTCCTTCGCGCAGGTGCTGCTGCTGAAGGAGCTGGTGC 307
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GAGTGTGAGAGGCTGTGCGAGCGCGCGCGGAAGAACGTGTGCTGGCTTCGGCTTCGC 367
GAGTGTGAGAGGCTGTGCGAGCGCGCGCGGAAGAACGTGTGCTGGCTTCGGCTTCGC 360
TGCTGACGGGGCCCGCGGGGGCCCCCGAGGCCCTTCACCAACAGCGTGGCGAGCTA 427
TGCTGACGGGGCCCGCGGGGGCCCCCGAGGCCCTTCACCAACAGCGTGGCGAGCTA 420
TGCCCAACACGGTGACCGACGCTGCGGGGGAGCGGGGCTGGGGGCTGCTGCTGCG 487
TGCCCAACACGGTGACCGACGCTGCGGGGGAGCGGGGCTGGGGGCTGCTGCTGCG 480
GCGTGGCGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
GCGTGGCGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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CTCCAGTGGCCCTACAGGTGTGGGGGGCGCGCTGTACAGCTCGCGCTGCCAC 600
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Db 2821 GCCGGCCACAGGCTATTCCCTGGTGGCGCCTGCTGGATACCCGGAGCC
QY 2852 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCT
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCT
QY 2912 CGGCTTCAAGGCTGGAGGAAACATGCGTCGCAAACTCTTTGGGGCTTTGGCGG
Db 2941 CGGCTTCAAGGCTGGAGGAAACATGCGTCGCAAACTCTTTGGGGCTTTGGCGG
QY 2972 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCA
Db 3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCA
QY 3032 CAAGATCCTCCTGCTGAGGCGGTACAGGTTTTCAGCATGTGTGCTGCAGTCC
Db 3061 CAAGATCCTCCTGCTGAGGCGGTACAGGTTTTCAGCATGTGTGCTGCAGTCC
QY 3092 TCAGCAAGTTTGGAAAGAACCCACATTTTCTGCGCGTCTCATCTCTGACACGG
Db 3121 TCAGCAAGTTTGGAAAGAACCCACATTTTCTGCGCGTCTCATCTCTGACACGG
QY 3152 CTGCTACTCCATCCTGAAAGCAAGAACGCAAGGATGTGCTGGGGGCCAAGG
Db 3181 CTGCTACTCCATCCTGAAAGCAAGAACGCAAGGATGTGCTGGGGGCCAAGG
QY 3212 CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGTGTGCCACCAAGCATTTCCCTGC
Db 3241 CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGTGTGCCACCAAGCATTTCCCTGC
QY 3272 GACTCGACACCGTGTCACTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCC
Db 3301 GACTCGACACCGTGTCACTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCC
QY 3332 GCTGAGTCGGAAGCTCCCGGGGACGACGTGACTGCTGGAGGCCGAGCCA
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGTGACTGCTGGAGGCCGAGCCA
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTTGAGTGTGATGGCCACCCGCCACAGCC
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTCTGAGTGTGATGGCCACCCGCCACAGCC
QY 3452 GAGCAGACACAGCAGCCCTGTACGCGCGGCTCTACGTCCCAGGGAGGGAGG
Db 3481 GAGCAGACACAGCAGCCCTGTACGCGCGGCTCTACGTCCCAGGGAGGGAGG
QY 3512 CACACCCAGCCCGCACCGTGGGAGTCTGAGGCCCTGAGTGTGTTGGCCG
Db 3541 CACACCCAGCCCGCACCGTGGGAGTCTGAGGCCCTGAGTGTGTTGGCCG
QY 3572 CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCC
Db 3601 CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCC
QY 3632 GAGTGTCCAGCACACCTGCCCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTC
Db 3661 GAGTGTCCAGCACACCTGCCCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTC
QY 3692 GGGCCAGCTTTCTTCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAG
Db 3721 GGGCCAGCTTTCTTCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAG
QY 3752 CCAGATTCGCCATTGTTTCAACCCCTGCCCTGCCCTCTTTCCTTCCACCCCC
Db 3781 CCAGATTCGCCATTGTTTCAACCCCTGCCCTGCCCTCTTTCCTTCCACCCCC
QY 3812 AGGTGGAGACCTTGAGAAGGACCTTGGAGCTCTGGGAATTTGGAGTGACCAA
Db 3841 AGGTGGAGACCTTGAGAAGGACCTTGGAGCTCTGGGAATTTGGAGTGACCAA
QY 3872 CCCTGTACACAGGCGAGGACCTTGACCTGGATGGGGTCCCTGTGGGTCAAA

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AGGTGCTGTGGGAGTAAATACTGAATATATAGAGTTTTCAGTTTGAATAAAA 4015

standard; cDNA; 4015 BP.

3 (first entry)

merase reverse transcriptase cDNA.

reverse transcriptase; TERT: enzyme; RNA interference;
rfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
ressive; antiinfertility; fungicide; antiparasitic;
matory; human; gene therapy; gene; ss.

ns.

Location/Qualifiers
56.3454
/*tag= a
/product= "TERT"

85-A2.

3.

2; 2002WO-US033146.

1; 2001US-0345326P.

2; 2002US-0359196P.

2; 2002US-0383195P.

IV ROCHESTER.

403289/38.
342063.

ic acid encoding or comprising interfering RNAs which target
RNA, useful for inhibiting telomerase activity for treating
fertility and disorders of the immune system.

; Fig 3; 52pp; English.

; sequence is that of human telomerase reverse transcriptase
A. The invention relates to the discovery that double-stranded
RNAs, such as short interfering RNAs (siRNA), which target
RNA or TERT mRNA are capable of inhibiting telomerase
inhibition of telomerase in cancer cells leads to telomere
end-to-end chromosomal fusion, and apoptosis. Interference of
activity can also be used for treatment of infertility, for
on or sterilisation, for immunosuppression, for treatment of
site and fungal infections, and in antiinflammatory therapies.
ise is active in a limited number of cell types, e.g. tumour
line cells, certain stem cells of the haematopoietic system, T
; sun-damaged skin, and proliferative cervix, most normal
ot affected by telomerase RNA interference therapy

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

98.2%; Score 3933; DB 7; Length 4015;
ilarity 99.1%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 36; Gaps 1;

AGCGTGCCTCCTGTGCGCACGTGGGAAGCCCTGGCCCCCGCCACCCCGGATGCC 67

Db 1 GCAGCGCTCGTCTCTGTGCGACGTGGGAAGCCCTGGCCCCCGGCCACCCCCC
Qy 68 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGTGCGAGCACTACCGC
Db 61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGTGCGAGCACTACCGC
Qy 128 GCGCGTGGCCACGTTCTGTGCGCGCCTGGGGCCCCAGGGCTGGCGGTGGT
Db 121 GCGCGTGGCCACGTTCTGTGCGCGCCTGGGGCCCCAGGGCTGGCGGTGGT
Qy 188 GGACCCCGCGGCTTCCGCGCGCTGGTGGCCCCAGTGCCTGGTGTGCGTCCC
Db 181 GGACCCCGCGGCTTCCGCGCGCTGGTGGCCCCAGTGCCTGGTGTGCGTCCC
Qy 248 ACGGCCCGCCCCCGCCCTCTTCCGCCAGTGTCTCTGCCTGAAGGAG
Db 241 ACGGCCCGCCCCCGCCCTCTTCCGCCAGTGTCTCTGCCTGAAGGAG
Qy 308 CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGGAGAAAGTGTGCGCTTCC
Db 301 CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGGAGAAAGTGTGCGCTTCC
Qy 368 GCTGTGGACGGGGCCCCCGGGGGCCCCCCCCAGGCTTCAACACAGCGTGC
Db 361 GCTGTGGACGGGGCCCCCGGGGGCCCCCCCCAGGCTTCAACACAGCGTGC
Qy 428 CCTGCCCAACACGTTGACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGC
Db 421 CCTGCCCAACACGTTGACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGC
Qy 488 CCGCGTGGGCGACGAGCTGTGTTTCACTGTGSCACGCTGCGCGCTCTTTG
Db 481 CCGCGTGGGCGACGAGCTGTGTTTCACTGTGSCACGCTGCGCGCTCTTTG
Qy 548 GGCTCCCAGCTGCGCTACCAAGTGTGCGGGCGCGCGCTGTACCAAGCTCGGC
Db 541 GGCTCCCAGCTGCGCTACCAAGTGTGCGGGCGCGCGCTGTACCAAGCTCGGC
Qy 608 TCAGGCGCGGCCCCCGCCACACGCTAGTGAGCCCCGAAAGCGCTGGGATGCG
Db 601 TCAGGCGCGGCCCCCGCCACACGCTAGTGAGCCCCGAAAGCGCTGGGATGCG
Qy 668 CTGGAACCAATAGCTCAGGAGCGCGGGTCCCTGGGCTGCCAGCCCCGG
Db 661 CTGGAACCAATAGCTCAGGAGCGCGGGTCCCTGGGCTGCCAGCCCCGG
Qy 728 GAGGCGGGGCGAGTCCAGCCGAAAGTGTGCGCGTTCGCCAAGAGGCCAGGC
Db 721 GAGGCGGGGCGAGTCCAGCCGAAAGTGTGCGCGTTCGCCAAGAGGCCAGGC
Qy 788 TGCCCCCTGAGCGGAGCGGACGCGCTTGGGCGAGGGTCTCTGGGCCACCCCGG
Db 781 TGCCCCCTGAGCGGAGCGGACGCGCTTGGGCGAGGGTCTCTGGGCCACCCCGG
Qy 848 GCGTGGACCGAGTACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCCGCG
Db 841 GCGTGGACCGAGTACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCCGCG
Qy 908 CACTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCCAACCCATCCGTGG
Db 901 CACTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCCAACCCATCCGTGG
Qy 968 GCACACGCGGGCCCCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGC
Db 961 GCACACGCGGGCCCCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGC
Qy 1028 CCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAGGAGC
Db 1021 CCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAGGAGC
Qy 1088 GCGCTCCTTCTACTCAGCTCTCTGAGGCCCGAGCTGAGTGGCGCTCGGAGGCT

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JTGACGATATCCACAGGGCTTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCC 2160
JCGCCTGAGCTGTA-----CATCCCCCA 2191
JCGCCTGAGCTGTA-----CATCCCCCA 2220

QY 2192 GGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTA
Db 2221 GGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTA
QY 2252 TCGGTATGCCGTGGTCCAGAAAGCCGCCATGGGCACGTCCGCAAGGCCTTCA
Db 2281 TCGGTATGCCGTGGTCCAGAAAGCCGCCATGGGCACGTCCGCAAGGCCTTCA
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Db 2341 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACC
QY 2372 GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGAGCTCCTCCCTGAATG
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Db 2461 CAGTGGCCTCTTCGACGTCTTCTCCTACGCTTCATGTGCCACCAAGCGGTGGCA
QY 2492 CAAGTCCCTACGTCCAGTCCAGGGATCCCGAGGGCTCCATCCCTCACCACGC
Db 2521 CAAGTCCCTACGTCCAGTCCAGGGATCCCGAGGGCTCCATCCCTCACCACGC
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QY 2612 GCTCCTGCTTGGTGGATGATTTCTTGTGTGGTACACCTCACCTCACCCACG
Db 2641 GCTCCTGCTTGGTGGATGATTTCTTGTGTGGTACACCTCACCTCACCCACG
QY 2672 CTTCCTCAGGACCTTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAAT
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QY 2972 TCACAGCCTGTTTCTGGATTTGCGAGGTGAACAGCCTCCAGACGGTGGCACCA
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QY 3032 CAAGATCCTCTGCTGCGGGCTACAGGTTTCAAGCATGTGTGCTGAGCTCC
Db 3061 CAAGATCCTCTGCTGCGGGCTACAGGTTTCAAGCATGTGTGCTGAGCTCC
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QY 3152 CTGCTACTCCTCATCCTGAAAGCCAAAGACGAGGGATGTGCTGGGGCCAAAGG
Db 3181 CTGCTACTCCTCATCCTGAAAGCCAAAGACGAGGGATGTGCTGGGGCCAAAGG
QY 3212 CGGCCCTCTGCCCTCCGAGGCGCTGAGTGGCTGTGCCACCAAGCATTCCTGC
Db 3241 CGGCCCTCTGCCCTCCGAGGCGCTGAGTGGCTGTGCCACCAAGCATTCCTGC

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CAGATTGCCCATTTGTTACCCCTCGCCCTGCCCTCCTTTGCCCTTCCACCCCCACCATCC 3811
|||||
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|||||
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|||||
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|||||
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|||||
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|||||
AGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015

standard; cDNA; 4015 BP.

```
} (first entry)
```

nerase reverse transcriptase encoding cDNA SEQ ID NO:1.

merase reverse transcriptase; enzyme; hTERT; chromosome 5;
antiulcer; epithelial cell migration promoter; wound;
tion; skin wound; lesion; burn; surgical incision; ulcer;
cell; keratinocyte; epidermal; mucosal; gene; ss.

28.

```
Location/Qualifiers
56. .3454
/*tag= a
/product= "human te
```

3-A2.

PD	21-NOV-2002.	
XX		
PF	09-MAY-2002; 2002WO-US014867.	
XX		
PR	09-MAY-2001; 2001US-0289903P.	
XX		
PA	(GERO-) GERON CORP.	
XX		
PI	Jiang X, Chiu C, Harley CB;	
XX		
DR	WPI; 2003-120591/11.	
DR	P-PSDB; ABP56676.	
XX		
PT	Composition for treating wounds and enhancing epithelialization c	
PT	surface, comprises vector encoding telomerase reverse transcripti	
PT	telomerized epithelial cells on a microparticle or a matrix.	
XX		
PS	Disclosure; Page 31-32; 68pp; English.	
XX		
CC	The present invention describes a pharmaceutical composition (
CC	comprising a vector encoding telomerase reverse transcriptase	
CC	an excipient or device, or comprises telomerised epithelial ce	
CC	microparticle or a matrix suitable for topical administration	
CC	administration to a wound site. (I) has vulnery and antiulce	
CC	activities and can be used to promote epithelial cell migratic	
CC	useful for treating a wound and enhancing epithelialisation of a	
CC	surface. The wound is especially skin wound including acute le	
CC	as traumatic lesion, burn, or surgical incision, chronic lesc	
CC	chronic venous ulcer, diabetic ulcer or compression ulcer and	
CC	is further monitored for closure. The telomerase activity or	
CC	expression is increased in epithelial cells at the site of tre	
CC	also in fibroblasts or endothelial cells at the site of treat	
CC	epithelial cells are especially keratinocytes. A polynucleotid	
CC	hERT is useful for the preparation of a medicament for treatm	
CC	wound or an epithelial surface in a human or animal. An epithe	
CC	with increased telomerase activity or increased expression of	
CC	useful for preparation of a medicament for the treatment of a	
CC	human or animal. (I) is also useful for treating wounds of oth	
CC	epidermal surfaces including mucosal surfaces such as bronchus	
CC	nose, oesophagus, stomach, or intestine. The present sequen	
CC	human hERT (hERT), which is given in the exemplification of t	
CC	invention. hERT is located to chromosome 5	
XX		
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;	
	Query Match 98.2%; Score 3933; DB 7; Length 4015;	
	Best Local Similarity 99.1%; Pred. No. 0;	
	Matches 3979; Conservative 0; Mismatches 0; Indels 36;	
QY	8 GCAGCGCTCGCTCCTGCTGGCACGTGGGAAGCCCTGGCCCGGCCACCCCCG	
Db	1 GCAGCGCTCGCTCCTGCTGGCACGTGGGAAGCCCTGGCCCGGCCACCCCCG	
QY	68 GCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGTGCGCAGCCACTACCGCG	
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QY	128 GCCGTGGCCACGTTGTCGCGCGCCCTGGGGCCCGCAGGGCTGGCGGTGGTGC	
Db	121 GCCGTGGCCACGTTGTCGCGCGCCCTGGGGCCCGCAGGGCTGGCGGTGGTGC	
QY	188 GGACCCGGCGGCTTTCCGCGCGGTGGTGGCCAGTGCCCTGGTGTGCGTGCCCT	
Db	181 GGACCCGGCGGCTTTCCGCGCGGTGGTGGCCAGTGCCCTGGTGTGCGTGCCCT	
QY	248 ACGGCCGCCCCCGCGCCCTCCCTTCCGCCAGGTGTCTCTGCCTGAAGGAGC	
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QY	308 CCGAGTGTGCAGAGGCTGTCCGAGCGCGCGCGCGAAGAACGTGTGGCCTTCG	
Db	301 CCGAGTGTGCAGAGGCTGTCCGAGCGCGCGCGCGAAGAACGTGTGGCCTTCG	

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Db 3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAA
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Db 3961 GAGTGTCTGCGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAA

RESULT 14
ACC44482
ID ACC44482 standard; DNA; 4015 BP.
XX
AC ACC44482;
XX
DT 29-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase gene.
XX
KW Gene; ds; human; telomerase reverse transcriptase; adipogenic
KW primary preadipocyte cell; adipogenesis; obesity; adipocytokin
XX anorectic; adiponectin; insulin.
OS Homo sapiens.
XX
FH Location/Qualifiers
FT CDS
FT 56..3454
FT /*tag= a
FT /product= "telomerase reverse transcriptase"

WO2003031640-A2.
PD 17-APR-2003.
XX
XX 07-OCT-2002; 2002WO-US031635.
XX
PR 06-OCT-2001; 2001US-0327650P.
PR 06-OCT-2001; 2001US-0327651P.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Kirkland J, Tchkonian T;
XX
DR WPI; 2003-421278/39.
DR P-PSDB; ABR58045.
XX
PT New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assa
PT clinical applications, and in the administration of therapeutic
PT particularly for obesity.
XX
PS Disclosure; Page 11-13; 53pp; English.
XX
CC The invention relates to the generation of primary preadipocyte
CC strains that expresse telomerase reverse transcriptase (TERT-
CC catalytic subunit of telomerase), and maintain and/or enhance ;

and maintain adipogenic capacity of the cell. This sequence the gene encoding the TERT protein. The cell strain can be search to study all aspect of adipogenesis, especially in researching treatments for e.g. obesity. The cell can also be identify adipogenesis modulators for use as therapeutic agents mones, growth factors, cytokines, enzymes, cholesterol binding cholesterol removing proteins or their combinations. ply, the therapeutic agent may be an adipocytokine, preferably 1, or insulin

115 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
nilarity 98.2%; Score 3933; DB 7; Length 4015;
Conservative 0; Mismatches 0; Indels 36; Gaps 1;
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2 09:53:30 2004

us-09-424-686f-9.rng

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RESULT 15
AAZ08150
ID AAZ08150 standard; cDNA; 4015 BP.
XX
XX AAZ08150;
XX AC
XX
DT 17-JAN-2000 (first entry)

merase reverse transcriptase cDNA.

merase reverse transcriptase; hTERT; telomerase; hEST2;
protein component; cell proliferative capacity;
tality; neoplastic phenotype; diagnostic application;
application; telomerase related condition; cancer;
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ns.

Location/Qualifiers
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9; 99WO-US007160.

8; 98US-00052919.

RON CORP.
IV TECHNOLOGY CORP.

Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
?

610834/52.
Y28881.

polynucleotides for human telomerase reverse transcriptase used
sing or treating cancer.

ig 1; 31pp; English.

t sequence encodes for human telomerase reverse transcriptase
is is the catalytic protein component of telomerase and is also
o as hEST2. This correlates with cell proliferative capacity,
tality, and the development of a neoplastic phenotype. Human
nse oligonucleotides are useful for diagnostic or prognostic
ns to telomerase related conditions, including cancer. They are
l as therapeutic agents, for inhibition of telomerase
and activity

015 BP; 663 A; 1364 C; 1274 G; 714 T; 0 U; 0 Other;

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99.1%; Pred. No. 0;
Conservative 0; Mismatches 1; Indels 36; Gaps 1;

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